

SPLICE FORM 1 (cDNA sequence):

1 GTGAGTCATA TGAAAGCTCC ACGCTGCTGA CCTCTGGCAA AAAGGGAGAG
51 AACAAAGGATA GGAGAGGCAG TGGGGGAAAG GTTCAAGTGC GGGTTTCTC
101 CTTGAACCTA GAAGATTATG GGTCAAGAGC TGTGTGCAA GACTGTACAG
151 CCTGGATGCA GCTGCTACCA TTGTTCAGAG GGAGGGAGG CACACAGCTG
201 TCGGAGGAGT CAGCCTGAGA CCACGGAGGC TGCCTTCAAG CTAACAGACC
251 TAAAAGAACG ATCATGTTCC ATGACTTCAT TTCACCCCAG GGGACTTCAA
301 GCTGCCCGTG CCCAGAAGTT CAAGAGTAA AGGCCACGGA GTAACAGTGA
351 TTGTTTCAAG GAAGAGGATC TGAGGCAGGG TTTTCAGTGG AGGAAGAGCC
401 TCCCTTTGG GGCAGCCTCA TCTTACTTGA ACTTGGAGAA GCTGGGTGAA
451 GGCTCTTATG CGACAGTTA CAAGGGGATT AGCAGAATAA ATGGACAAC
501 AGTGGCTTTA AAAGTCATCA GCATGAATGC AGAGGAAGGA GTCCCATTAA
551 CAGCTATCCG AGAACGTTCT CTCCTGAAGG GTTTGAAACA TGCCAATATT
601 GTGCTCTGCG ATGACATAAT CCACACCAAA GAGACACTGA CATTGTTTT
651 TGAATACATG CACACAGACC TGGCCCAGTA TATGTCAG CATCCAGGAG
701 GGCTTCATCC TCATAATGTC AGACTTTCA TGTTTCAACT TTTGCGGGGC
751 CTGGCGTACA TCCACCACCA ACACGTTCTT CACAGGGACC TGAAACCTCA
801 GAACTTACTC ATCAAGTCACC TGGGAGAGCT CAAACTGGCT GATTTGGTC
851 TTGCCCGGGC CAAGTCCATT CCCAGCCAGA CATACTTTTCA AGAAGTCGTG
901 ACCCTCTGGT ACCGGCCCCC TGATGCTTTG CTGGGAGGCC CTGAATATT
951 CTCTGAGCTG GACATATGGG GTGCAGGCTG CATCTTTATT GAAATGTTCC
1001 AGGGTCAACC TTTGTTTCTT GGGGTTTCCA ACATCCTTGA ACAGCTGGAG
1051 AAAATCTGGG AGGTGCTGGG AGTCCCTACA GAGGATACTT GGCCGGGAGT
1101 CTCCAAGCTA CCTAACTACA ATCCAGGTAA TATTGATCTG AGCTTTGAA
1151 TACTCTGAGA ATTAGTAATG TAAGGAGAGC ATTGGCCACG CTAACAGGGC
1201 GTTCTTGTAT TGTGAACTCA GCGGCAAAGA TGGGTGTAGA GGAATTCTA
1251 CATTCAATATA TTCCCTGACT AATCTTGTG TGAGGAAGAC ACTGAAAGAG
1301 TAGCTGAGGT TAGACCAGTT CCCCAGCTCT GTAAAACACA AGTAGCAAGC
1351 TGAATAGAAAT TTGAAATGAC TATTACTGTG GATTCCACAT CCATTGTC
1401 ATACCCAATG GCTCAAAGA ACAACTCAA AGATGGGCTC ACTTTGGGC
1451 CCCCTGACTG TCATAAGTGT ATTGATTAGT ATTGAATTGC ATATGTATAA
1501 AAAGAAAGCT AATGCAACAG AACAGAGGT GAGGCTCGCT AGGCCTAGGA
1551 CATGCCAAGT AAGCTGTCTG TAGGTTATAC TTACTAAGAG TTCATTCA
1601 GCCTGTAAAC CTGACACTTG GTCATTGTCT CTCACACATT TCATCTTCA
1651 AGACTGGCTT CTGGGATCGA TTTAGAAGTG CTGGAAGTGT TATCCATGGG
1701 GGAATTCTTT GAGAAGCTGT CGCAGGGCCA CATCAGAGGG ATCAGATTAA
1751 GCAGTAGTCA CTTCAAGGAT GTTGAGACAG AGGGGAGGAG ACAGGCACTG
1801 AACTACAGGA TGAAGGATCA TATTAGAAGC TGAAGAAGCA AATAAAGCCC
1851 ATGCCAAAGC TGAGCTCTCA CTGGCAGGGT TGAAGGGGAG GTAGAAAGGT
1901 ACAGATAACG ACAAGATTAG GGTGGATATG CTCCAAGCCA GATTTTCTA
1951 GTCTTATGG TCTTACATTG TTCCATTACT AAAAATGAAA TCTTCCCAA
2001 TTGTTGTCCT TACTTTTTTT TTTTTTTTTT GAGATGGAGT TTTGCTCTTA
2051 TCGCCCAGGC TGGAGTGCAG TGAGCCGAGA TTGCGCCACT GCATGTCCGC
2101 AGTCCGACCT GGGCGACAGA GCGAGACTCC GTCTAAAAC TAAAAAA
2151 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2201 AAA (SEQ ID NO:1)

FEATURES:

5'UTR: 1-117
Start Codon: 118
Stop Codon: 1147
3'UTR: 1150

SPLICE FORM 2 (transcript sequence):

1 ATGGGTCAAG AGCTGTGTGC AAAGACTGTA CAGCCTGGAT GCAGCTGCTA

FIGURE 1A

```

51 CCATTGTTCA GAGGGAGGCG AGGCACACAG CTGTCGGAGG AGTCAGCCTG
101 AGACCACGGA GGCTCGTTC AAGCTAACAG ACCTAAAAGA AGCATCATGT
151 TCCATGACTT CATTCAACCC CAGGGGACTT CAAGCTGCC GTGCCAGAA
201 GTTCAAGAGT AAAAGGCCAC GGAGTAACAG TGATTGTTTT CAGGAAGAGG
251 ATCTGAGGC A GGGTTTCAG TGGAGGAAGA GCCTCCCTT TGGGGCAGCC
301 TCATCTTACT TGAACTTGGA GAAGCTGGGT GAAGGCTCTT ATGCGACAGT
351 TTACAAGGGG ATTAGCAGAA TAAATGGACA ACTAGTGCT TTAAAAGTCA
401 TCAGCATGAA TGCAGAGGAA GGAGTCCCAT TTACAGCTAT CCGAGAAGCT
451 TCTCTCCTGA AGGGTTGAA ACATGCCAAT ATTGTGCTCC TGCATGACAT
501 AATCCACACC AAAGAGACAC TGACATTCTG TTTGAATAC ATGCACACAG
551 ACCTGGCCC GTATATGTCT CAGCATTCCAG GAGGGCTTCA TCCTCATAAT
601 GTCAGACTTT TCATGTTCA ACTTTTGCAGG GGCCTGGCGT ACATCCACCA
651 CCAACACGTT CTTCACAGGG ACCTGAAACC TCAGAACTTA CTCATCAGTC
701 ACCTGGGAGA GCTCAAACCTG GCTGATTTG GTCTTGCCTG GCCAAGTCC
751 ATTCAGCAGCC AGACATACTC TTCAGAAGTC GTGACCCCT GTTACCGGCC
801 CCCTGATGCT TTGCTGGGAG CCACTGAATA TTCCCTCTGAG CTGGACATAT
851 GGGGTGCAGG CTGCATCTT ATTGAAATGT TCCAGGGTCA ACCTTTGTTT
901 CCTGGGGTTT CCAACATCCT TGAACAGCTG GAGAAAATCT GGGAGGTGCT
951 GGGAGTCCCT ACAGAGGATA CTTGGCCGGG AGTCTCCAAG CTACCTAACT
1001 ACAATCCAGA ATGGTTCCA CTGCCTACGC CTCGAAGCCT TCATGTTGTC
1051 TGGAACAGGC TGGCAGGGT TCCTGAAGCT GAAGACCTGG CCTCCAGAT
1101 GCTAAAAGGC TTTCCCAGAG ACCCGTCTC CGCCAGGAA GCACTTGTTC
1151 ATGATTATTT CAGGCCCTG CCATCTCAGC TGTACCAGCT TCCTGATGAG
1201 GAGTCTTTGT TTACAGTTTC AGGAGTGAGG CTAAAGCCAG AAATGTGTGA
1251 CCTTTGGCC TCCTACCAGA AAGGTACCA CCCAGCCAG TTTAGCAAAT
1301 GCTGGTGA (SEQ ID NO:4)

```

FEATURES:

Start Codon: 1

Stop Codon: 1306

Homologous proteins:

Top 10 BLAST Hits

Score E

SPLICE FORM 1:

CRA 18000005115058 /altid=gi 6755044 /def=ref NP_035204.1 PFTA...	391	e-107
CRA 18000005205923 /altid=gi 6912584 /def=ref NP_036527.1 PFTA...	390	e-107
CRA 18000005100533 /altid=gi 2392814 /def=gb AAB70455.1 (U6239...)	389	e-107
CRA 151000011260745 /altid=gi 12002201 /def=gb AAG43234.1 (AF1...	386	e-106
CRA 1000682315356 /altid=gi 5579351 /def=gb AAD45514.1 (AF1524...	367	e-100
CRA 89000000195020 /altid=gi 7292375 /def=gb AAF47781.1 (AE003...)	367	e-100
CRA 1000682315355 /altid=gi 5579349 /def=gb AAD45513.1 (AF1524...	367	e-100
CRA 1000682315353 /altid=gi 5579343 /def=gb AAD45510.1 (AF1523...)	367	e-100
CRA 1000682315354 /altid=gi 5579347 /def=gb AAD45512.1 (AF1524...)	367	e-100
CRA 1000682315352 /altid=gi 5579341 /def=gb AAD45509.1 (AF1523...)	367	e-100

SPLICE FORM 2:

CRA 18000005115058 /altid=gi 6755044 /def=ref NP_035204.1 PFTA...	469	e-131
CRA 18000005205923 /altid=gi 6912584 /def=ref NP_036527.1 PFTA...	468	e-131
CRA 18000005100533 /altid=gi 2392814 /def=gb AAB70455.1 (U6239...)	467	e-131
CRA 151000011260745 /altid=gi 12002201 /def=gb AAG43234.1 (AF1...	465	e-130
CRA 1000682315356 /altid=gi 5579351 /def=gb AAD45514.1 (AF1524...)	422	e-117
CRA 1000682315355 /altid=gi 5579349 /def=gb AAD45513.1 (AF1524...)	422	e-117
CRA 1000682315354 /altid=gi 5579347 /def=gb AAD45512.1 (AF1524...)	422	e-117
CRA 1000682315353 /altid=gi 5579343 /def=gb AAD45510.1 (AF1523...)	422	e-117
CRA 1000682315352 /altid=gi 5579341 /def=gb AAD45509.1 (AF1523...)	422	e-117
CRA 18000005045994 /altid=gi 1524004 /def=emb CAA67862.1 (X995...)	421	e-116

FIGURE 1B

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

BLAST dbEST hits:

Score	E	
SPLICE FORM 1:		
gi 9806331 /dataset=dbest /taxon=960...	1334	0.0
gi 2140968 /dataset=dbest /taxon=9606 ...	575	e-162
gi 2028058 /dataset=dbest /taxon=9606 ...	377	e-102
gi 13132599 /dataset=dbest /taxon=960...	319	8e-85

FIGURE 1C

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

SPLICE FORM 2:

gi 9806331 /dataset=dbest /taxon=960...	1334	0.0
gi 2140968 /dataset=dbest /taxon=9606 ...	954	0.0
gi 2028058 /dataset=dbest /taxon=9606 ...	377	e-102
gi 2140870 /dataset=dbest /taxon=9606 ...	283	5e-74

EXPRESSION INFORMATION FOR MODULATORY USE:

SPLICE FORM 1:

library source (from BLAST dbEST hits):
gi|9806331 Uterus-endometrium adenocarcinoma cell line
gi|2140968 testis
gi|2028058 Lung fibroblast cell line
gi|13132599 Kidney renal cell adenocarcinoma

Tissue Expression:

whole brain

SPLICE FORM 2:

library source (from BLAST dbEST hits):
gi|9806331 Uterus endometrium adenocarcinoma line
gi|2140968 Testis
gi|2028058 Lung fibroblast
gi|2140870 Testis

FIGURE 1D

SPLICE FORM 1:

1 MGQELCAKTV QPGCSCYHCS EGGEAHSCR SQPETTEAAF KLTDLKEASC
51 SMTSFHPRGL QAARAQKFKS KRPRSNSDCF QEEDLRQGFQ WRKSLPFGAA
101 SSYLNLEKLG EGSYATVYKG ISRINGQLVA LKVISMNAEE GVPFTAIREA
151 SLLKGLKHAN IVLLHDIIHT KETLTFVFYE MHTDLAQYMS QHPGGLHPHN
201 VRLFMFQLLR GLAYIHHQHV LHRDLKPQNL LISHLGELKL ADFGLARAKS
251 IPSQTYSSSEV VTLWYRPPDA LLGATEYSSE LDIWGAGCIF IEMFQQQPLF
301 PGVSNILEQL EKIWEVLGVP TEDTWPVGSK LPNYPNGNID LSF (SEQ ID
NO:2)

SPLICE FORM 2:

1 MGQELCAKTV QPGCSCYHCS EGGEAHSCR SQPETTEAAF KLTDLKEASC
51 SMTSFHPRGL QAARAQKFKS KRPRSNSDCF QEEDLRQGFQ WRKSLPFGAA
101 SSYLNLEKLG EGSYATVYKG ISRINGQLVA LKVISMNAEE GVPFTAIREA
151 SLLKGLKHAN IVLLHDIIHT KETLTFVFYE MHTDLAQYMS QHPGGLHPHN
201 VRLFMFQLLR GLAYIHHQHV LHRDLKPQNL LISHLGELKL ADFGLARAKS
251 IPSQTYSSSEV VTLWYRPPDA LLGATEYSSE LDIWGAGCIF IEMFQQQPLF
301 PGVSNILEQL EKIWEVLGVP TEDTWPVGSK LPNYPNGNID LSF (SEQ ID NO:5)

FEATURES:

Functional domains and key regions:

SPLICE FORM 1:

[1] PDO00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 2

1 27-29 SCR
2 70-72 SKR

[2] PDO00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 3

1 31-34 SQPE
2 75-78 SNSD
3 279-282 SELD

[3] PDO00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

108-114 KLGEWSY

[4] PDO00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 8

1 2-7 GQELCA
2 59-64 GLQAAR
3 98-103 GAASSY
4 112-117 GSYATV
5 126-131 GQLVAL
6 141-146 GVPFTA
7 155-160 GLKHAN

FIGURE 2A

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

8 244-249 GLARAK

[5] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature

109-132 LGEGSYATVYKGISRINGQLVALK

FIGURE 2B

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

[6] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature

220-232 VLHRDLKPQNLLI

[7] PDOC00170 PS00191 CYTOCHROME_B5_1
Cytochrome b5 family, heme-binding domain signature

188-195 YMSQHPGG

SPLICE FORM 2:

[1] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 3

1	27-29	SCR
2	70-72	SKR
3	343-345	TPR

[2] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 4

1	31-34	SQPE
2	75-78	SNSD
3	279-282	SELD
4	377-380	SAQE

[3] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

108-114 KLGEGSY

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 8

1	2-7	GQELCA
2	59-64	GLQAAR
3	98-103	GAASSY
4	112-117	GSYATV
5	126-131	GQLVAL
6	141-146	GVPFTA
7	155-160	GLKHAN
8	244-249	GLARAK

[5] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature

109-132 LGEGSYATVYKGISRSQLVALK

[6] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature

FIGURE 2C

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

220-232 VLHRDLKPQNLLI

FIGURE 2D

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

[7] PDOC00170 PS00191 CYTOCHROME_B5_1
Cytochrome b5 family, heme-binding domain signature

188-195 YMSQHPGG

Membrane spanning structure and domains:
(SPLICE FORMS 1 & 2)

Helix	Begin	End	Score	Certainty
1	283	303	0.776	Putative

FIGURE 2E

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

BLAST Alignment to Top Hit:

SPLICE FORM 1:

>CRA|18000005115058 /altid=gi|6755044 /def=ref|NP_035204.1|

PFTAIRE

protein kinase 1 [Mus musculus] /org=Mus musculus
/taxon=10090 /dataset=nraa /length=469
Length = 469

Score = 391 bits (993), Expect = e-107

Identities = 184/240 (76%), Positives = 208/240 (86%)

Frame = +1

Query: 406

FGAASSYLNLEKLGEGSYATVYKGISRINGQLVALKVISMNAEEGVPTAIREASLLKGL 585
FG A SY LEKLGEGSYATVYKG S++NG+LVALKVI + EEG

PFTAIREASLLKGL

Sbjct: 129

FGKADSYEKLEKLGEGSYATVYKGSKVNGKLVALKVIRLQEEEGTPPTAIREASLLKGL 188

Query: 586

KHANIVLLHDIIHTKETLTTFEYMHDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIH 765
KHANIVLLHDIIHTKETLT VFEY+HTDL QYM QHPGGLHP

NV+LF+FQLLRGL+YIH

Sbjct: 189

KHANIVLLHDIIHTKETLTTFEYVHTDLCQYMEQHPGGLHPDNVKLFLFQLLRGLSYIH 248

Query: 766

HQHVLHRDLKPQNLLISHLGEKLADFGGLARAKSIPSQTYSSEVVTLWYRPPDALLGATE 945
+++LHRDLKPQNLLIS GELKLADFGGLARAKS+PS TYS+EVVTLWYRPPD

LLG+TE

Sbjct: 249

QRYILHRDLKPQNLLISDTGELKLADFGGLARAKSVPSHTYSNEVVTLWYRPPDVLLGSTE 308

Query: 946

YSSELDIWGAGCIFIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPVGSKLPNYNP 1125
YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPVG

LP++ P

Sbjct: 309

YSTCLDMWGVGCIFVEMIQGVAAFPGMKDIQDQLERIFLVLGTPNEDTWPVGVHSLPHFKP 368
(SEQ ID NO:6)

>CRA|18000005205923 /altid=gi|6912584 /def=ref|NP_036527.1|

PFTAIRE

protein kinase 1 [Homo sapiens] /org=Homo sapiens
/taxon=9606 /dataset=nraa /length=451
Length = 451

Score = 390 bits (990), Expect = e-107

Identities = 184/245 (75%), Positives = 209/245 (85%)

Frame = +1

Query: 406

FGAASSYLNLEKLGEGSYATVYKGISRINGQLVALKVISMNAEEGVPTAIREASLLKGL 585

FIGURE 2F

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

FG A SY LEKLGEGLSYATVYKG S++NG+LVALKVI + EEG
PFTAIREASLLKGL
Sbjct: 111
FGKADSYEKLEKLGEGLSYATVYKGSKVNGKLVALKVIRLQEEEGTPFTAIREASLLKGL 170

Query: 586
KHANIVLLHDIIHTKETLTTFEYMHDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIH 765
KHANIVLLHDIIHTKETLT VFYEY+HTDL QYM +HPGGLHP
NV+LF+FQLLRGL+YIH
Sbjct: 171
KHANIVLLHDIIHTKETLTLCQYMDKHPGGLHPDNVKLFLFQLLRGLSYIH 230

Query: 766
HQHVLHRDLKPQNLLISHLGELKLAQFGLARAKSIPSQTYSSEVVTLWYRPPDALLGATE 945
+++LHRDLKPQNLLIS GELKLAQFGLARAKS+PS TYS+EVVTLWYRPPD
LLG+TE
Sbjct: 231
QRYILHRDLKPQNLLISDTGELKLAQFGLARAKSVPSTSNEVVTLWYRPPDVLLGSTE 290

Query: 946
YSSELDIWGAGCIFIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPVGSKLPNYP 1125
YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPVG
LP++ P
Sbjct: 291
YSTCLDMWGVGCIFVEMIQGVAAPGMKDIQDQLERIFLVLGTPNEDTWPVGHSLPHFKP 350

Query: 1126 GNIDL 1140
L
Sbjct: 351 ERFTL 355 (SEQ ID NO:7)

SPLICE FORM 2:
>CRA|18000005115058 /alt=id=gi|6755044 /def=ref|NP_035204.1|
PFTAIRE
protein kinase 1 [Mus musculus] /org=Mus musculus
/taxon=10090 /dataset=nraa /length=469
Length = 469

Score = 469 bits (1195), Expect = e-131
Identities = 225/330 (68%), Positives = 270/330 (81%)

Query: 97
FGAASSYLNLEKLGEGLSYATVYKGISRNGQLVALKVISMNAEEGPFTAIREASLLKGL 156
FG A SY LEKLGEGLSYATVYKG S++NG+LVALKVI + EEG
PFTAIREASLLKGL
Sbjct: 129
FGKADSYEKLEKLGEGLSYATVYKGSKVNGKLVALKVIRLQEEEGTPFTAIREASLLKGL 188

Query: 157
KHANIVLLHDIIHTKETLTTFEYMHDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIH 216
KHANIVLLHDIIHTKETLT VFYEY+HTDL QYM QHPGGLHP
NV+LF+FQLLRGL+YIH
Sbjct: 189
KHANIVLLHDIIHTKETLTLCQYMEQHPGGLHPDNVKLFLFQLLRGLSYIH 248

FIGURE 2G

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

Query: 217

HQHVLHRDLKPQNLLISHLGEKLADFGLARAKSIPSQTYSSEVTLWYRPPDALLGATE 276
+++LHRDLKPQNLLIS GELKLADFGLARAKS+PS TYS+EVVTLWYRPPD

LLG+TE

Sbjct: 249

QRYILHRDLKPQNLLISDTGELKLADFGLARAKSVPSTSNEVVTLWYRPPDVLLGSTE 308

Query: 277

YSSELDIWGAGCIFIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPVGSKLPNYP 336
YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPGV

LP++ P

Sbjct: 309

YSTCLDMWGVGCIFVEMIQGVAAPGMKDIQDQLERIFLVLGTPNEDTWPVGVHSLPHFKP 368

Query: 337

EWFPLPTPRSLHVWNRLGRVPEAEDLASQMLKGPRDRVSAQEALVHDYFSALPSQLYQ 396
E F + + +SL WN+L V AEDLAS++L+ P++R+SAQ AL H+YFS

LP +L++

Sbjct: 369

ERFTVSSKSLRQAWNKL SYVNHAEDLASKLLQCSPKNRLSAQAALSHEYFSDLPPRLWE 428

Query: 397 LPDEESLFTVSGVRLKPEMCDLLASYQKGH 426

L D S+FTV VRL+PE + + ++ K +

Sbjct: 429 LTDMESSIFTVPNVRLQPEAGESMRAFGKNN 458 (SEQ ID NO:8)

>CRA|18000005205923 /alt=id=gi|6912584 /def=ref|NP_036527.1|

PFTAIRE

protein kinase 1 [Homo sapiens] /org=Homo sapiens
/taxon=9606 /dataset=nraa /length=451
Length = 451

Score = 468 bits (1191), Expect = e-131

Identities = 224/330 (67%), Positives = 270/330 (80%)

Query: 97

FGAASSYLNLEKLGEWSYATVYKGISRINGQLVALKVISMNAEEGPFTAIREASLLKGL 156
FG A SY LEKLGEWSYATVYKG S++NG+LVALKVI + EEG

PFTAIREASLLKGL

Sbjct: 111

FGKADSYEKLEKLGEWSYATVYKGSKVNGKLVALKVIRLQEEEGTPFTAIREASLLKGL 170

Query: 157

KHANIVLLHDIIHTKETLTFVFEYMHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIH 216
KHANIVLLHDIIHTKETLT VFEY+HTDL QYM +HPGGLHP

NV+LF+FQLLRGL+YIH

Sbjct: 171

KHANIVLLHDIIHTKETLTVFEYVHTDLCQYMDKHPGGLHPDNVKLFLFQLLRGLSYIH 230

Query: 217

HQHVLHRDLKPQNLLISHLGEKLADFGLARAKSIPSQTYSSEVTLWYRPPDALLGATE 276
+++LHRDLKPQNLLIS GELKLADFGLARAKS+PS TYS+EVVTLWYRPPD

LLG+TE

Sbjct: 231

QRYILHRDLKPQNLLISDTGELKLADFGLARAKSVPSTSNEVVTLWYRPPDVLLGSTE 290

FIGURE 2H

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

Query: 277

YSSELDIWGAGCIFIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPVGSKLPNYP 336
YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPGV

LP++ P

Sbjct: 291

YSTCLDMWVGICIFVEMIQGVAAFPGMKDIQDQLERIFLVLGTPNEDTWPVGVHSLPHFKP 350

Query: 337

EWFPLPTPRSLHVWNRLGRVPEAEDLASQMLKGFPDRVSAQEALVHDYFSALPSQLYQ 396
E F L + ++L WN+L V AEDLAS++L+ P++R+SAQ AL H+YFS

LP +L++

Sbjct: 351

ERFTLYSSKNLRQAWNKL SYVNHAEDLASKLLQCSPKNRLSAQAALSHEYFSDLPPRLWE 410

Query: 397 LPDEESLFTVSGVRLKPEMCDLLASYQKGH 426

L D S+FTV VRL+PE + + ++ K +

Sbjct: 411 LTDMSSIFTVPNVRLQPEAGESMRAFGKNN 440 (SEQ ID NO:9)

>CRA|18000005100533 /altid=gi|2392814 /def=gb|AAB70455.1|
(U62391)

PFTAIRE kinase [Mus musculus] /org=Mus musculus
/taxon=10090 /dataset=nraa /length=423
Length = 423

Score = 467 bits (1190), Expect = e-131

Identities = 224/330 (67%), Positives = 269/330 (80%)

Query: 97 FGAASSYLNLEKLGEGLSYATVYKGISRINGQLVALKVISMNAEEGPFTAIREASLLKGL 156
FG A SY LEKLGEGLSYATVYKG S++NG+LVALKVI + EEG PFTAIREASLLKGL

Sbjct: 83 FGKADSYEKLEKLGEGLSYATVYKGSKVNGKLVALKVIRLQEEEGTPFTAIREASLLKGL 142

Query: 157 KHANIVLLHDIIHTKETLT VFEYMHDLAQYMSQHPGGLHPHNVRLFMFQLLRLAYIH 216

KHANIVLLHDIIHTKETLT VFEY+HTDL QYM +HPGGLHP NV+LF+FQLLRLGL+YIH

Sbjct: 143 KHANIVLLHDIIHTKETLT VFEYVHTDLCQYMDKHPGGLHPDNVKLFLFQLLRLGLSYIH 202

Query: 217 HQHVLHRDLKPQNLLISHLGEKLADFGLARAKSIPSQTYSSEVTLWYRPPDALLGATE 276
+++LHRDLKPQNLLIS GELKLADFGLARAKS+PS TYS+EVTTLWYRPPD LLG+TE

Sbjct: 203 QRYILHRDLKPQNLLISDTGELKLADFGLARAKSVPSTSNEVTLWYRPPDVLLGSTE 262

Query: 277 YSSELDIWGAGCIFIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPVGSKLPNYP 336

YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPGV LP++ P

Sbjct: 263 YSTCLDMWVGICIFVEMIQGVAAFPGMKDIQDQLERIFLVLGTPNEDTWPVGVHSLPHFKP 322

Query: 337 EWFPLPTPRSLHVWNRLGRVPEAEDLASQMLKGFPDRVSAQEALVHDYFSALPSQLYQ 396

E F + +SL WN+L V AEDLAS++L+ P++R+SAQ AL H+YFS LP +L++

Sbjct: 323 ERFTVYNSKSLRQAWNKL SYVNHAEDLASKLLQCSPKNRLSAQAALSHEYFSDLPPRLWE 382

Query: 397 LPDEESLFTVSGVRLKPEMCDLLASYQKGH 426

L D S+FTV VRL+PE + + ++ K +

Sbjct: 383 LTDMSSIFTVPNVRLQPEAGESMRAFGKNN 412 (SEQ ID NO:10)

FIGURE 2I

Hmmer search results (Pfam):

SPLICE FORM 1:

Model	Description	Score
E-value	N	
PF00069	Eukaryotic protein kinase domain	247.7
1.6e-70	1	
CE00031	CE00031 VEGFR	14.3
0.0002	1	
CE00359	E00359 bone_morphogenetic_protein_receptor	7.1
0.25	1	
CE00022	CE00022 MAGUK_subfamily_d	6.0
0.11	1	
CE00287	CE00287 PTK_Eph_orphan_receptor	-59.4
0.00019	1	
CE00292	CE00292 PTK_membrane_span	-61.0
1.9e-05	1	
CE00286	E00286 PTK_EGF_receptor	-76.4
1.9e-06	1	
CE00291	CE00291 PTK_fgf_receptor	-87.0
0.00095	1	
CE00290	CE00290 PTK_Trk_family	-100.0
1.4e-08	1	
CE00016	CE00016 GSK_glycogen_synthase_kinase	-152.6
3.5e-08	1	
CE00288	CE00288 PTK_Insulin_receptor	-196.5
0.0012	1	

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00022	1/1	204	231 ..	126	153 ..	6.0	0.11
CE00359	1/1	222	247 ..	274	299 ..	7.1	0.25
CE00031	1/1	204	247 ..	1051	1094 ..	14.3	0.0002
CE00290	1/1	106	307 ..	1	282 []	-100.0	1.4e-08
CE00288	1/1	106	310 ..	1	269 []	-196.5	0.0012
PF00069	1/1	103	326 ..	1	220 [.]	247.7	1.6e-70
CE00286	1/1	103	335 ..	1	263 []	-76.4	1.9e-06
CE00287	1/1	104	335 ..	1	260 []	-59.4	0.00019
CE00016	1/1	1	340 [:]	1	433 []	-152.6	3.5e-08
CE00292	1/1	104	341 ..	1	288 []	-61.0	1.9e-05
CE00291	1/1	104	341 ..	1	285 []	-87.0	0.00095

FIGURE 2J

Docket No.: CL001098DIV II
 Serial No.: TO BE ASSIGNED
 Inventors: YAN, Chunhua et al.
 Title: ISOLATED HUMAN KINASE ...

SPLICE FORM 2:

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	263.6	2.6e-75	1
CE00031	CE00031 VEGFR	14.3	0.0002	1
CE00359	E00359 bone_morphogenetic_protein_receptor	7.1	0.25	1
CE00022	CE00022 MAGUK_subfamily_d	6.0	0.11	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-42.5	3.2e-14	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-55.2	0.0001	1
CE00292	CE00292 PTK_membrane_span	-63.9	2.8e-05	1
CE00286	E00286 PTK_EGF_receptor	-76.4	1.9e-06	1
CE00291	CE00291 PTK_fgf_receptor	-88.8	0.0012	1
CE00290	CE00290 PTK_Trk_family	-94.9	6.1e-09	1
CE00288	CE00288 PTK_Insulin_receptor	-196.5	0.0012	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00022	1/1	204	231 ..	126	153 ..	6.0	0.11
CE00359	1/1	222	247 ..	274	299 ..	7.1	0.25
CE00031	1/1	204	247 ..	1051	1094 ..	14.3	0.0002
CE00288	1/1	106	310 ..	1	269 []	-196.5	0.0012
CE00286	1/1	103	335 ..	1	263 []	-76.4	1.9e-06
CE00292	1/1	104	335 ..	1	288 []	-63.9	2.8e-05
CE00291	1/1	104	339 ..	1	285 []	-88.8	0.0012
CE00290	1/1	106	354 ..	1	282 []	-94.9	6.1e-09
CE00287	1/1	104	367 ..	1	260 []	-55.2	0.0001
PF00069	1/1	103	387 ..	1	278 []	263.6	2.6e-75
CE00016	1/1	1	434 [.]	1	433 []	-42.5	3.2e-14

FIGURE 2K

1 TATAGGCCAA TGCTGTGGCT CACGCGTGT A TCCCAGCAC TTTGGGAGGC
51 AGGAGGATCG CTTGAGCTCA GGAATTGGAG ACAAGCCTAC GTAACATAGT
101 GAAACCTCTG TCTGTACAAA TAATAAAAGA ATTTTCAGG CATGGTGGCG
151 TGCACCCCCA GTGCCAGCTA TTTGGGAGGC TGAGGTAGGA GGAATGCTTG
201 AAGCCAGGAG TTGAAGACAA GCCTAGGCAA CATAGTGAGA CCCTGTGTCT
251 ATAAAAAATA ATTAGCTGGT TGTCTGGCA CAGGCCGTGCA GCTAGCTACT
301 CGGAAGACTG AGGTGGAGG ATCACTGAGC CCAGGAGGCT GAGGCTGCAG
351 TGAACAGTGA TCACCCAGCT GGATTCAGC CTGGAAGACA GAGGGAGACC
401 CTGTTTCCAA AAAAAAAA AAAAAAAAT GCAAGAAAAG ACATCATAAA
451 CTTGACCTGG GACATAACTT TTATGTGATG AAATTCAAA TCTTTTAGGA
501 AGAAATTAGC ATTTCTGATA AAATGTATTA TAATTATATT ATTATAAATT
551 CAAATGGAAT TAAATATTCT GAGAAACTAG CTTCTCACTC TCTCAGTTGT
601 CAGTCAAAC TTTAATGGTC TTTGGCCGGG TGCGGTGGCT CACGCCGTGTA
651 ATCCCAGCAC TTGGGAGGC CGAGGCCGGT GGATCACAAG GTAGGAGAT
701 CGAGACCATC CTGGCTAAC A CGGTGAAACC TCGTCTCTAC TAAAATACA
751 AAAAATTAGC CGGGTGCGGT GCCAGACGCC TGATGCTCCA GCTGCTCAGG
801 AGGCTGAGGC AGGAGAATGG TGTGAACCCG GGAGGCGGAG CTTGCAGTGA
851 GCCGAGATTG CGCCACTGCA CTCCAGCCTG GGCAGACTG CGAGACTCTG
901 TCTCAAAAAA AAAAAAAA AAAAGTTGAA TGTTCTTTGA GCCAAGTAGT
951 CTTCCCTTTTCT TTCTTCTTCT TTTTTTTTT TTTCAAAAAA ATATCTCTAG
1001 ATTGAATCTT GGAATTGGCT TAAGTCTCTT CTCTGTGGC AATTTGAAA
1051 TGAAAAAATA CATGCTCATA ATTAAATTAC CTGAACATTT TAAAAAACCA
1101 TCATGAGGTT CAAATATCAA ATATTCTAA ATATTGTTGT GATAATAGAC
1151 ATAACCTTTA TTTTTTCCCT TAATAATGAT TGTTTATATA TCCTCCATT
1201 TGTCTCACTT TATGATTAGT ATATTATAGT GGCAATAATC TTAGGAATCT
1251 AACAGAGAAA AGTGTGCA TTGAAGACTA CAGACTGCAA ACCAATTAA
1301 GCCAGATTCC TTGACATGTT GTGCTGTTAA TATAGTACTT TACATATAGT
1351 AAACATTAAT TACATATATG TGGAGGAAG CAAGCAAGAA AGGAAGAAAG
1401 TATTCATTC AAACTCCTCT CTCTCCATCA CCATTGGCTA ATATCATCAT
1451 TTGTACAGTT AAGAACAAACA TAGGTGCTCA CCACATAGTT TTTGAATAAA
1501 TGAATGAATG GCAACCCCTTC TAAGACTATT GGATACACTA TTGTTTGAAG
1551 GCAAAGAGAT GCAGTAGATA TTTCAACTT TTTCTGTGTT TTATGATTCT
1601 GTGGTTTCTT TGACTACTAA AAGTTAGCTA GGTAGCAAAT TTGTTTAAA
1651 GTCTGAAAAC CAAAATGCTT TCAGATAAAA GGTAGGGAGA AAAATACTCC
1701 TCAACATGTC CACTTTAGCA CCAGGAAAAC CTAATATCAA TATCACC
1751 AATGATATCA TATAAATATC ATTGCTAGA TAAGCAATGT CAATCCCTAA
1801 AAACTATGTA TACCAATAGC ACTAACTTGT GGCCAGAACAGAAC
1851 CTGTGCCAAA TTTTATTCTA TTCAATAACA GCTGCTCGT TTTCAGTTGT
1901 GCACATCTGA ATGCAAGCAA TCCCTGTCTG ATGTGGAGTT TCTTGCAG
1951 ATAAGGAAAA ACTGCTGAAG TTGTGAGGCT GCTCCAGGCA GAGCCATCAT
2001 GTGAGTCATA TGAAAGCTCC ACGCTGCTGA CCTCTGGCAA AAAGGGAGAG
2051 AACAAAGGATA GGAGAGGAG TGGGGGAAAG GTTCAAGTGC GGGTTTCTC
2101 CTTGAACCTA CAAGATTATG GGTCAAGAGC TGTGTGCAA GACTGTACAG
2151 CCTGGATGCA GCTGCTACCA TTGTTAGAG GGAGGCGAGG CACACAGCTG
2201 TCGGAGGAGT CAGCCTGAGA CCACGGAGGC TGCGTTCAAG GTATTTGTAT
2251 CCCAGGAGAG AGCATCTTC TCTATTGATA AACCAAGGAG TTCAGACACT
2301 CCCTTTTGT AGCAGGGATCT GATTCTCTG CGGTAGGTCT AAACCAATAA
2351 AATGAAAATT CTATTAAAGT CACAGAAAAT TTATGGCTGT AGTTATCAA
2401 TTTGGGAAAT TTCTTGTAAA CAAAAGGGA AAAATAATCC TTGGCTTTGG
2451 GCTGCACGAA ACTCACTTGG CTTGAAGTCG AGAAAGTAGT TCTCTAAAAA
2501 TCTCTAAGGT CCTAAATTAC AGAGCTGAAA CTTAAAAGGC AAGCTGCAGT
2551 ATTAGTTGGT ATGCTATGGA TTTGAAACTT TAGTAATTAG TTCATGATTA
2601 TTAGCAATGC CATAGATTAT TCCCCTACAG CAATAAAATTA AGTGGACATG
2651 AAAAAAAA GCCAGACTTA AACAGAAAAA AGTTGAAAAA CATCCATCAA
2701 AGAGATTTAG GTTAACCTGA ATGTTAAAGA CACATTTTA GGTGAAGAAA

FIGURE 3A

2751 GAATGTAGTA TTTCAGGAGT TGATACCATT ATGGTCTTT TCAGGGATCT
2801 TTCAAGAAAA GTGCCTTTG GGGGTACAGG AAGCTTAGAA AACATTTGAA
2851 GAGTGAAAAT GAGGCAAATA AAGAAAAAAT GGTTCACCA GGCACGTAA
2901 CTTTACTTTG CATAAATTT ATTCTGCTC TTTCTTTT CTCTAGCTAA
2951 CAGACCTAAA AGAACATCA TGTTCCATGA CTCATTCA CCCCAGGGGA
3001 CTTCAAGCTG CCCGTGCCA GAAGTCAAG AGTAAAAGGC CACGGAGTAA
3051 CAGTGATTGT TTTCAGGAAG AGGATCTGAG GCAGGGTTT CAGTGGGTGA
3101 GTGAGCAGCT GATGTTGATC AAGAAGAATT TAATGTGAGC TTGTCTACGG
3151 AGGCCGGCCC TTGCTTCCAG GGCAATTACT GAGCGAGCCT TCCCAAGTCT
3201 GCTCTGGCAA TGCTGTCTAA TTTCCCTGGG GAAAAAAAAGT CAACACTAAA
3251 AAAAAGTGT CTTTCTCTC TCCCTTCAC CCGCTCCTT TCCCCATTCC
3301 CCTAGAGCAG AGGAAGAGCC TCCCTTTGG GGCAGCCTCA TCTTACTTGA
3351 ACTTGGAGAA GCTGGGTGAA GGCTCTTATG CGACAGTTA CAAGGGGATT
3401 AGCAGGTGAG TGACACATAG CTGGGAGAGA CTTTAGAGAT GAGAGTCCC
3451 CCCCCCAAT TTCATATTAT AAAGCCAGGT GAGACATCAT AGAAGTTCAT
3501 AGCACTCAGG ACCTGTGCAA GACACCATGG CCGACAGGGA GAGAGACATG
3551 ATAACCTAAA CAGCCTTGAA AGAAAAACAA ACCTGCCCTG CCCTAATTAA
3601 AATCAGCCC CTTAAATGTT TATCAGCCT TCCCTTCTT CATTCAATT
3651 AGAGAATTCA AAGAAAATAG ACATTCTCTA CTACTGACCC AAAGAACAAAT
3701 TATCACTCTT CAGGCCCTGTG GGAGGCACAG TTGGTAAAGC GTCTCTAAC
3751 GGTTTTTAT ATCCCTCCCT AAATCACAAT GACAGAGTT TGTAATGGCA
3801 ACCTGGAATT TGCTGCTTC TCCCTCCACC TGGCCTTTAT AGAAGAAACT
3851 GAAGTTGGTT TCTGCAAATT ATGGTACATG CAAAAGATGA TAAATCCTAG
3901 ATTTTTATA TTTGCAAAAT ACACAAAATG TCTGGAGAAT AAAAATACTG
3951 CTTATCCAAA AGCTAAGTAC TAATTTGGT AAACAACCAA CTTGTTAAA
4001 TATATGTAAA AGATCCATGA ATTCCCCTT TAGTCAGGT GGGAAAGTTG
4051 GATGGTCGCT TTTTCTTTA TGTTACTCCA ATAGAGAGAA AAGTAATGGC
4101 TCAATAGTGG TAAATATTA ATTTAAAAAA TATAGCTGAT CCGAGTGCAG
4151 TGGTGTTCAC AACTACTTGA TCACAAACAG TTACAGATT CTTGTTCC
4201 TCTCCACTCC CACTGCTTC CTTAACTGGC CAAAACGAA AAAAGAAAAA
4251 TTTTATATAA CTACTACAAG ACTAAATATT TATTATTTT CTTAGTATT
4301 ATGCTGTTAT TATTATTTT ACTTGTAAA ACAGGATTGT AGGGGACATA
4351 CAGTTTATT TTATTTTATT ATTTATATAT TTATTTATT ATTTGGAAT
4401 GGAATCTCTG TCACCCACGC TGGAGTCAG TGGTGCAGTC TCAGATGACT
4451 GCAACCTCTG CCTCCTGAGT TCAAGCAACT CCTCTGCC C TGGCCCTTTA
4501 TACTTTCTTA ATCTGTTTA GTCATGGTGT ACCTTAACCT TTTCAATGC
4551 TGAGAACATC TGCAATAAAG GACCACATT TATTTTATT TAAGCTTC
4601 CATATCAATT TGGCCATGGT AACTGTTTC AAGGTGGTC GGAACGGGGG
4651 CACCCCTGGAA CATACTTGGG TACATGGGCA CCATGGACAC TTCTGATC
4701 CTCTTCTGAG TTCTGACTTT GATTGTTCTG CACAGACCTT TCCAGCCCC
4751 AGTTTACACA GAATTCACTT ATCTTTCTT CTAGTTACTT TATGTTTCT
4801 TTTTCATTTA ACTCTTTCAT CTACTGGAA TTATATTGT ATATTCAAA
4851 TCACCCCAGC TCCATTATT AGATTTCTT TTCTCTGATG GTTGAATG
4901 CTGCCATGAT TATATATTAG ATCTCACGAA TACTTGAAAT TCTTCTGTT
4951 CTAATCTTTT AAAATCATG TTTCCTTAAT CTATCTTTC TTATATTGT
5001 GCTGCATGAT TTTAATTATT GTTGCTTTAG GCTATTTTA GAATATATCA
5051 AAACTCTACG TTAGAGAATT ATTGACATCT TTGCAATTATT AGATTTCTA
5101 ATACAAATAT CCTGAAATA TCTAATACAA CAGTCTCTGG ATGGTC
5151 TACAAGACCC TATAGAATCC CTACCCCTCCA TTCCCCGGCA CACACTCAGC
5201 TCCTCCCTGT CCTCATCTCC TTCCCCCTCTC CTGCTTCAAT GACAGACTGC
5251 TCCTGCCTCA GTCAAGGACT TTTAACTTGC TGTTCCCT GCCTGGAGCT
5301 GCCTCCACT GTTCATGCAC ACAGCTGACT CCCCCCTGCC ATCAGATT
5351 TGGTTCAAGT GTTACCTTAT TTATAAAACT GTAGTCCCAG CTAGTCC
5401 GAGGCTGGAG GCAGGAGAAT CACTTGAAC T TGGAGGAG AGGTTGCAGT
5451 GAGCTGAGAT CGGCACCACCG GCACTCCAGC CTGGGTGAGA GTGACACTGT

FIGURE 3B

5501 CTCAAAAAAA AAAAAAAAGCA TTTTCTCTTA TAAACATATT TGCCAAAAAA
5551 CTTTTTGCA GGGTTGGGG AGAATTTCAC AGAACCATGT TCTGAGGAAA
5601 ATACTTACCT CATAAAACTC TAAAACAAAA TTTCAAAGAC ATGATAAGGC
5651 AAACAAAAGA AACTGGGGAA AAGTATATGC AAAATAGTTC AATAAAAAGG
5701 TGGGCAAATC GGCAAATCAC AAGAAAAACA GAAAAGATCC ATAAACTTAT
5751 GAAAAGTCAG TTTCACATAT GTTAAAGAA ATATAAATTA AAATGCGATA
5801 AACCTTTTA CTTTCAAAT AGGCCAAAAA AAAAAAGAAG ATGAAAGCGA
5851 AAAGCCAACC CACATGATAG GGCTATGACA GAGGGACACA GGAGCCAAC
5901 GAAAGAGCTT CCAAAGGACA AAGCTGCAA AATATGAGCA ACCAAAAAAA
5951 GTGGTATTAA ATTATAACCC AAAGTATAA ATAAATATCT ATGAGTCCGT
6001 ACTGATATAA ATAATGATT CAATACATTA ACAAAATGGGA GAGAAGAAC
6051 AAATCTCTA TGCCAAATAA ATACAAATAA TTATGTAGA TAATATACCT
6101 TCAAAGAGGT ACAGCATAAC TCTCCACTC TTAAGTGTGG GTCATTCTA
6151 GTGGCATTTC TCTAAAAGTA CAGTATGAA AAGGGGGAGA AAGAGTAAC
6201 TTAGAGTAGA GAAACCTGAC CAACACTATC TCAGACAGGT GACTAAGGTC
6251 AACATCAAAA GTCATAAATC ATGATGATGG TATGCACTCT TTTTTTTTT
6301 TTTTTTTTT TTCTCAGATG GAGTCTCACT CTGTCGCCA GGCTGGGTG
6351 CAGTGGCGCA ATCTCAGCTC ACTGCAACCT CGGGCTCCCG GGTCAGCG
6401 ATTCTCCTCT CAGCCTCTG AGTAGCTGG ATCACAGGCG CGTGCACCA
6451 TACCCGGCTA ATTTTTGTG TTTTAGTGA GACGGGGTTT CACCATGTTG
6501 CCCAGGCTGG TCTCAAATC CCGAGCTAG GCAATCCACC CACCTCAACC
6551 TCCCAAAGTG CTAGGATTAC AGGCATGAGC CACTGCGCT GGCTGAGGGT
6601 ATGCACTTT TTTTTTTTG AGACGGAGTC TTGCTCTGTC GCCCAGGCTG
6651 GAGTGCAGTG GCACGATCTT GGCTCACTGC AAGCTCCGCC TCCCAGGTT
6701 ACGCCATTCT CCTGCCCTAG CCTCCCCAGT AGCTGGACT ACAAGGTGCC
6751 CCACCACCCA CACCCGGCTA ATTTTTGTG TTTTTAGTAG AGACGGGGTT
6801 TCACTGTGTT AGGCAGGATG GTCTCGATCT CCTGACCTCC TGATCCACCG
6851 GCCTTCGCCT CCCAAAGTGC TGGGATTACA GGCCTGAGCC ACTGTGCCCG
6901 GCCTGATGAA ATGTTAAATC TTTATTAAAT ATCGGATTGT ACAAGAATGA
6951 ACTATAAGAG AAAAGTTACA TGGAGGAAAA AAGGTTACTA ACAATATGAT
7001 TTTAATCCCA CTGTATTAAA AACAATGGAT TTATACCTGC ATTTAAATCT
7051 TCTCTATTCT CAGCACTTAG CTGATATGAA TAAAATGATG AATGAGGGGA
7101 CAGTAGGAGG AAATGAAGAG AGAGAGAATA ATGGTGTGGC CTGGGAAGAT
7151 CAGGTAGCAC TTAGAAGCCC GCTGCAAGAA TTTGGCTTTT ATTCTAAGTA
7201 ATGCGTGGAG ATATGGTGGC TTTTGAACAG AAAAGTGAET TGTCTGATT
7251 GTCATTGAA AAGTATGCCT CCAACTACTA CTGCTGAGAG TAAATAGTAG
7301 GAGTGCAGT GTGCTCAGCA GGGAAACTGT TAGAAGACCA CTACAAGGCT
7351 GGGCTTGGTG GCTCGTCCT GTAACTCCAG CACTTGGGA GCCTGACGTG
7401 GGCAGATCAC CTGAGGTCAG GAGTTGAGA CCAGCCTGGC CAAAATGGTG
7451 AAACCCCCAT CTCTGCTAAA AATACAAAAA TTAGCCAGGT GTGGTGGGG
7501 TCCCCGTAA TCCCAGCTC TTGGGAGGCT GAGGCAGGAG AATTGCTTGA
7551 ACCCAGGAGG TGGAGGTTGC AGTGAGCCAA GATCGTGCCTA CTGTA
7601 GCCTGGCAA CAGAGCGAGA TTCTGTCCTA AAAAAAAAAA AAAAAAAACAA
7651 AAAAACAAAA AAACACTACA ATAAGTCAGA TGAAAAATAA TAATAAGCTC
7701 CAAATTTCT ATAATGGACA TATATATATA TATCACTTTA GTAAAGAGGG
7751 AAAATGCTTT GGAATATATA TGTTATATAT GTATTGATAC ATGTTAAACT
7801 TTTTATTTTG AGAAAATTAT AGATTTATAT GCTAGAATAT ATTTTGAAGT
7851 GAAAGTGCTT TTGTTAAGCC ATCTTGGTA TAAATTGCTG CTTTGAACCA
7901 CCTCAATAAG TGTGTGCCCT TCAATCCCTC TCTTCTAGAA TAAATGGACA
7951 ACTAGTGGCT TAAAAAGTC ACGCATGAA TGCAAGAGAA GGAGTCCCCT
8001 TTACAGCTAT CCGAGAAGGT AAGAACAGCA GAAATGGACC CAATAGATCT
8051 GTTTGAGTC CTTGATTTGG TAAAAAATGT ATTGCATTGA TCCATTCA
8101 ATCTAGTTT GATTCTCTG GAATACTATA ATTACATTT TATTTTCA
8151 ACAAGTTTT CAAGAAATT TACACTGCTAT TTTTATTACTT AATTTTGAGG
8201 AAATTGAGAT TTAAAACAT TATATCACTT GACCAAAACT ATAAATTCA

FIGURE 3C

8251 TGAGCAATT A CTAATAC TTT CCATGTGTT GGCCTCATGC TAGGTGCTAA
8301 GGCTATAACCT ATATAACCTC AGAAAATTCC TATAAAAGAG AAAATATATA
8351 ATCACACAAA TTCTTACTGG GAAATTGCC TGAACATAAC ATGTTGTTAG
8401 CTAGCACTTG GAGATTCTCC AGAAGGCATG CATGTTTAGT GTTACTGCCT
8451 GTATTTCTC TGTGCCCTGG ACAGTACAGC AAATGGGTGA GGAACCTGGT
8501 GTCAAATGGA CTTGGGTTTG CAGCACAGGT CCACCAATCA CTAGTGGTAT
8551 GATGTTGGGT AGGTTACTTT AGCTATTAT TACTCAGTTT CTTGCAGGAA
8601 GAGGATAATA GTGGTACCTA TTTCATGGAG TTGTTATGAG TATTCAACAA
8651 GAATATGTAT ATAAGCACT TATCACAGAG TCAGTTTTC AGAGTTCAAC
8701 AAATGTTGAC CATTTTATT CCATTCTTCT TTTCCTGGGT AATGTCTTAT
8751 TTACCATCAA GATAACTAAT ACTTTATAAC ATAAACATCA AGAACGCCAAC
8801 ATAGTGAAAT GAATCATTAA AAATATAATT TATCAACCTT TATTGCATGA
8851 GCCATTGAA ATAAGATGAT GATAGGATTG CTATGCATT CAGCAAATC
8901 CCAGAGAAAT GGCACCTCCC TGGCCTTATT TTCTCCACT TTTAACTACT
8951 TATCTTCTGT TCTTTACTGA GCACATGCTA TATGCAGAGT ATGCTGCTGG
9001 ATGCTGTGAA GGATGAGAAG AGAAACCCAT GTCTTGTTC TATCATTGCG
9051 AGTCTTAACA GAGCACATGA TTCAAGTTAC AAGTGTATAA AAGACATAAA
9101 CTAAGATGAG AGCAAGTTAG TCTCAGTGT ACTGATGGAG TCACTAGATT
9151 TTGAACGTGAG CTTGGAAGGA TAGGTTATGC AAACAAGCAT GGAAAAAGCA
9201 ATTCAAGAAAA TGAGTTTATA ACTGAATTG ATACCCTTT CAAAAGTCTT
9251 TCAGAGCCCC TGAGGAATAC ATCATTGTG ATTTAATTGG AAGGGCCAAA
9301 TGGGCTATTG GTTGTAGCCAG AGATTCTAC TGGTAGGATC AGGTGCATTC
9351 TGGGAGAAGG CATGGTTTA AGTGTAAAT ATAATGGAAA CTGCATTAAC
9401 TAATGTTACTT ATTAATGGTC TCCATGAAAG GATGATCAGA TTTGGAAAGA
9451 GATGTATGGA TAGGTTAAAG AGTATTGTG AACGTAATAG AAATCCCAG
9501 GTCACCCGCA TAAGAGGAAG GTTCTTTG TGAGCTTGAG TTTGCCAATT
9551 GCTTAAGATT GGCTTGTCTT AGATATTGCC CACAGCCAAG TTTTCAGGT
9601 TGACATTTAA CTGTAACAGT GAAACCTTTT GCCAGGTTG CTAACAGATG
9651 GTTCTCAGCA TGGTTCAGAA AACCTGGATC CGTTTCTTC TGTATGCTAA
9701 ATGTTTCTTT CATTGCAAT TTACGGAGGA ATTGCCTCTC CATCACAGGT
9751 GTTACAATT ACATTTAGTA GTCAACTGTG GACTTTCTTG GTTTGTTTA
9801 TGGACTTACC TTACCGAATG CTTTGTCTGT GTAATATTAA AAACCCACAAG
9851 AGGATTCTG ACACATTGGA GGTGTTAGG ATCCAATTT CCAACAATGA
9901 ATGTTTCTTT TTACACCACT ATAAAAGCTT GGAGCCCTTG TTAAAAGAGC
9951 CCTCTCCCT CAAGAAGATA TGAGGCTTTA TTCGAAAACT TTGGCACTGT
10001 CCCATTTTC CTGTAAGAAC TTTAAGGATG TGAGACCAGG GAGACAGGAG
10051 GTTAAATGAG AAGGGCTGGA AGGCAAAGTA AGAACAGCTG GAGTTCTTA
10101 GCTAAAATCC AGGGTCACTA GCTAAAAGG CAACCGAAAG GCACGTGCG
10151 GAAAACGTGAA CAAGTAATGC AGCCCTCTT AAAAAGCCTT GAAGCAGGAA
10201 TTGCTTTCC TGAACAATT GGCTGCCCTG ATGGTATAGC AGCCAAAGAT
10251 TTATTAAGTA TGATTTACT ACATATATGG TCTCTTTCTA TACAGGTAGA
10301 ATACATGTGG CAATTTACTA GTCTGGTCAT TTGGAGTACT ATTTTCATT
10351 GACCTTAACA TGTGATATTA TGAAACTAGC AAAAGTATGA ACAGCACTAA
10401 GGAACATTTT TTTTTTTT TTTTGAGACG AAGTTTGCT CTTGTTGCC
10451 AGGCTGGAGT GCAATGGCAC AATCTTGGCT TACTGCAACC TCTGCCCTCG
10501 GGGTTCAAGC AATTCTCCTG CCTCAGCCTC CGGAGTAGCT GGGATTACAG
10551 GCATGTGCCA CCACACCCAG CTAATTGT ATTTTAGTA GAGACAGGGT
10601 TTCCCCATGT TGGCCAGGCT GGTCTTGAAC TCCTGACCTC AAGTGATCTG
10651 CGTGTCTCAG CCTCCCAAGG GAAATATATC TTAATACATG TGTCACTGCT
10701 TTTCATACTT CTTTCAATCC TCTTAACAAT CTTTAGAGAT AGATATTATT
10751 AATATTATTC CACTATATGG TGGTGATTCA AACCAAATCT CTCTGATTCA
10801 AAAATTCTATA GGCTTTCTAC GCACCCACTG TAGAAATATT CATTAGCAC
10851 CTACTATGAC CAGGTACTCT GCCGAACTGC TAGATACACA GCAATACACA
10901 AAATAGATGT GTTCCCTACC ACCCTCATTC CTTGCTAAT TAAGAAAAGC
10951 AGAGGCCTTC ATAGTGCCTT GGAAATCTCT CATAATTGAC TCTAGAATTG

FIGURE 3D

11001 TATTTTAAGT GTTGATTTTT ACAACTAGGA GGAAATACCT TCATTTGAAT
11051 AGGCTAATGT GTTATGTTTT TACATAGTAC AACATTTCTT AGTTTTATGA
11101 AACTTTATAG CAATATCTTA ATATAATGTG CATTGTTTA AATATTTTG
11151 TTCAAGTGGT CAACTTTGG TTTAAACTGA GGACTTTCA GCGTAAATA
11201 GCATTTTCT TAGGAAGGAG TCATATAACT AATCTTTTT GAGGACAAGG
11251 CATATGACAT AATCTCCCCC TTCCCTTACA TAATGTATAT TTTTAAAACC
11301 TTTATACCAA CCCTAGGAAG TAAAATGTGC TATTTTTGTT GTAGAGATAA
11351 AGAAAATTCTA GCCTCAGAGA GGTTAGTTAA CTTGTCTGAG GTCACAGAGA
11401 TAGTAATCAG AGTTGTTAGA ATCCATTCT ATTCTATTTA AAATCCCTTC
11451 TACTTTATTA TGATGAATT GGAAATGCTT AACTAAAGTA TTTATTGTTT
11501 AGCAACAGTA AAAATAAAAAA TAGAAATCTG TTTTTTATTAT ACATTTTATA
11551 TAAACGTTAA GGAAAATGCA GAAGAAGTAT TTTTTTAATC TTTAATTTTA
11601 GATTCAAGGG GTACATGTCC AGGTTGTTA CATGAGTATA TTGATGATG
11651 CTGAGGTATC TTGTCACCCA AATAGTGAGT ATAGTACCTG ATAGGTAGTT
11701 TTTCAACCCG TGTCCCTCTC CCTTCCCTCTC CCCTTTTGGG GTCCCTGGTG
11751 TAGTGTCTAT TATTCCCATC TTATGTCTGT GTGTTCCCAA TACCCCCAGT
11801 TATTAGCTTT CACTGTAAAG TGAGAACATG TGGTATTGTT TTTCTGTTCC
11851 TGGGTTAATT CACTTAGGAT AATGGCCTCC ATCTGCATCC ATGTTGCTGC
11901 TAAGGAAATG GTTTTTTTT TTTTTTTTT TTGTGGCTGC ATAGTGTTTT
11951 ATGGTGCCAG TGTACAAATT TTCTTATCC AATCCACCAT TGCTGGCAC
12001 CTAGGTTGAG TCCATGTCTT TGCTATTGTG AATAGTGTG TGACGAACAT
12051 AAAAGTCTAG GTGTCTTTTT GACAGAACGA TTTATTTTCC TTTGGGTATA
12101 TACCCAGGAA TGGAATTGCT GGGTCAAATG GTAATTCTGT TTTTGGTTTT
12151 TTTGAGGCAG GAGATGGGAC TCGACTCCAG AGATGGGCT TGAACACTAA
12201 ACCAAATTTA GGACTAGCCA AAACAGGGCC TGGGGGGAGG CAGCTTCCA
12251 GAAGACACAC CCACCAAGTGT GCCATGTCAG TTTACCATTG CCATGGCAAC
12301 ACCTGAAAGT TACCACCCCT TCCCGTAGCA ACAACCTGAC AACCTGGAAT
12351 TACCACTCTT TTCCCTAAAC TTTCTGCATA AACTGCCCT TAATTGCAT
12401 ATAACAAAAA GTGGGTATAA ATATAACTGT AGAGCTACCT ATGAGCTGCT
12451 ACTCTGGGCA CACTGCCTAT GTGGCAGCCC TGCTCTGCAA GGAGAGGTAC
12501 ACCCGCTGCT GCTGAACACT GCTGCTTCAA TAAAAGCTGC TGTCTAACAC
12551 CACAGGCTCA CCCTTGAATT CTTTCTGGG TGAAGCCAAG AACCCCTCCA
12601 GGCTAAGCCC CAGTTTGGG ACTTGCCTGC CCTGCCTCAC TTTGAGAAAT
12651 TTCTAAACTG TTTTCCACAG TGGCTGAAC TATTAAACATT CCCACCCACA
12701 GTGTATAAGC ACTCCCTTT CTTCTCAAGC TTACCAAGCAT CCATTAACCT
12751 TTTACTTCTA AATAATAGCC TTTTGACTG GTGTGAGATG GTATCTCATT
12801 GAGGTTTGTG TTTGCATTT TCTGATGATT CGTGATGTT AGCAATTTTT
12851 TCATATGTTT GTTGGCCACT TGTGTGCCA AAAGAAATAT TTTAAAGAAA
12901 ATAATACATC ATGTTGTATA TTCACTCAATT CTGATTCTAT CATTGATTCT
12951 ACAGTGCCGG TAATTGCAGT GTTTAAATTA GAAACAGTCT CAGCTAAGAA
13001 TCTTTTAAGA TCATTCTCTA GTAGAAAAC ATTACAAAGT AATGATTCCC
13051 AATCCATATA TGAGAAAACT GAGCCAAAAA TAGGCTAAGG AGCCTCCCTA
13101 AGGTCTACAC ATGAGGCAGG GGAGGAGGCT GATTAGAACT TCTGAATTGC
13151 CAATGACCAC AAATAGTCTA GGGTAGGCCT GGTTGACAGA AAGTCTGCCA
13201 TTGAACACCA TCATATCACA TGACAAATAC AGCAAATTCA TTGTGCATAG
13251 TTACGTCTTT ATAAAACAAA ATAATGCCAG GATAATGGTA TGTGATCAGC
13301 ATTACAATTCT CAAAGATACC AAGACAACTA CTTATCTGAC ACTTGTCTTA
13351 GTATTTCTCT AACATTTATC TAAAATTATT TCAATTATTT CTTTCTCGG
13401 AATGCATAAC TTGACTCATT GACTTGATTG ATGATTCTCA GATCAAAGGA
13451 AATGTAACAA CAGGGACTAG AAACACTTTT TTATTCAATG TCCAATGAGG
13501 GTTGGGGAGG ACTCCATCAT TGACTCATT AATAATTCTT CATAAACTCA
13551 TTACAATTGG CCTGGCTTTC ATTAATTCTAT GAGCACTTAT TGAGCACCAC
13601 ATGCCAGGCC TGTGCTAGTG CTGGAGATGC AAAGACAAGG GCAAGTTCAA
13651 TCCATGCCCT CAATGAGTTT ACAGCCTAA GACGACTTTG ACTACCAGGC
13701 CTTCATTACA TAGAGCGACA TCCTAGGACT TGGAGAATCA GCTTTCTCT

FIGURE 3E

13751 GGAGCCTTAA AGACATCCCT ATTTACTTT GTGTCTTTTC TTTGAAGAAA
13801 AACAAAAATA AGTATACATA GGATACATTA ATAATAAAAAA AACAGTATT
13851 TATGAGACTC AGAACGCTAA TTTTAGGATC TTTGCCCTTC TCAGTTGACT
13901 TTTGTGTCCTC TCAACTGTTT AGTCTGCAGG ACAGATATCA CATCCTGCTG
13951 TGCAGTTTAT AAAATGTCCT TAAAATTAGA AGAAAGAAA GCCTTGTCTT
14001 CCTGGGTTTA AGACCCACAC ATCTGAGGCT GTAGGCATT CAGATCCCTC
14051 TGGTGGATGG ACCAAAATGA TAAACAATAC TGTGAGATAA ATGCTTTAAA
14101 CATCATCTGC TCTTTCATCT GAATTCCCTA TTCATTATTC GGCAACATTC
14151 ACAGTTTCA TATAACGATT TCAGTAGTTC TAGGGCACCA GAAAAGCAGT
14201 ACTAGGAATG GCCATAAAGC ATAGAATATT TATAATCTAA TGAGGGAGAC
14251 AACTAAAAGA AAGAAGGAAT AAAAGCATCT TCAACAGAAA CACCCTTAC
14301 CAACCAACTA GAGGTATAGA AATGATATTA GGTAAATTAGT GACCACTAAT
14351 TAAAGATAA ATATTTATTG AGTGCCAGAC ATTGTTCCAG GCACTGAGTA
14401 TATAGCAATA AGCAAAAAAA ACAAAACAAA ACAAAACAAA AGTGCCCAC
14451 CTCAAATGGAG TTTATATTCT CAATTGTGGA GACAGACAAT AAACAAATAT
14501 TTATATATAA AATGTCAGAT GGTGGTGACA GGCACATATGG AAAAGAATAA
14551 AGCAGGGCCC AGAGAGAGAG GGTAGGATGG GGTAGAGGTG GGATGGGTG
14601 GAGGGCTGCT GAGGTGGGAT GGAGTAGAGG GCTGCTATCT CACCTAGAAT
14651 GGTCAAGGAA GTCTGCACCT ATATGTATCA CTTGAGCGGA GGCTCTGAAG
14701 AAAGTGAGGG AGGATGAAGG CAGAGAGGTG AGAAGAGAGG ATTACAGGAA
14751 AAGACATTGG CAAGTGTAAA ATCCTGGGT GGAAATGTGT TTGCAAGTGT
14801 GTCTAAGGAA CAGCTAGGAG GCCAGTGAGG CTAAGCCA GTGAGCAAAG
14851 ATGGGAGTGT GAGGAGATGA CAGGTACGA TGGGCACAGC CAACAGTAGG
14901 GTGGGCAGGA AATCGCAAGT CCTTGAATT TACTCTGCAG GAGATGAGAG
14951 GCCACTGGAG GGTGGAAAC CAGGAGGCAC ATGCCCTAAC TCATTTGAGA
15001 AGGATAGCAG TGTCTGGCTG TCCTGTGAAG AAGTGGCCAT AGGAGGAAAG
15051 CAGGGAAAGCA GGCATTGCA ATAATTCAAGC CAACATATGA TAGTGGCTTG
15101 GTCCAGGGTG CTGGCAGAAG ATATGGCAAG GGAGGGGTTG TGGACAATT
15151 GGAAGGTAAT GCCAATAGAT TTGTATGTGA TAAAAAGTTG AGAGGACTTG
15201 ACGTGTACGA GTGGTTAAC TTCATAAAAT GGATGAATGG TTAAAAAGAT
15251 TTCCGAAAG AACTGTGGG TTGAAGGTA AACTAGTAAC TCCAATGTAA
15301 GTAACACAACA GAGAAATACA AAACAGACAT TTTCTACT CCTACAAAAA
15351 CTGTAATTAT CAAGAAGACG ACATGAAGTT TATACCCAGT ATTGTTAGCA
15401 GGAAGCCTCA TTCCAAGTAG ATATTTTCC TTGGCCATT TAGCAAGTGA
15451 GAGCATGAGG CCATCATAAT GAACAAATCA TGCCATCATG ATTAAAAAG
15501 AACATCTGG AGTTTAGTA ATATAGTTAG GTGAGACTAA AATTATACTA
15551 AACATAAAAT TAAAATATCT TAACAATATT CTTAGCAATT TCAGCTTAC
15601 CATATCCTT TGAAATCTAA TTTGCTATA TGCTTTGAA CATAGGGGTG
15651 GGGGAAAGAG AGAAATTAT GAGATAATT ATAATAAAA ATACACCTAA
15701 AGTATAAGCA TTCTCAACTG ATGGTCAGAA AATATGGAAG GTATTCAAAA
15751 CTCTAGCAGA AACATACCAT AAACAAGATT TTAAGACTGA AAGTAGACGT
15801 TTAGTGGGT TCAGGGTGAAG AGGCAGGGGC AAGAAGCTGG CAAGAAGAGG
15851 GAAGGGATAC TAATTCTAA TTGCCTCTGT AATGCTTTAC ATTACCAAG
15901 GTTCCACAAA TGGTATCTGA TTCCATCCTC ATATCAACCC TATGAAGTAA
15951 GTCAGAAAAG ACGATGTCTC TTTCCCTAAG GAATGAATTG AGACTTAGGT
16001 TGAGATACTC TCCAGAGCTT ACTCAGATAG GAAGTGACAG GGCCAGGATT
16051 CATATTAGGG CTTCTGGCTC CACAGACAGT TCTCCTTAAG ACTTTCAATA
16101 AATATGTTTGT ACAAAATTAAG TGCTTACTCT CGGCTGAGTG TGGTACTAGG
16151 TGGTGTGGCA GCATCTCAA AAGGGGAAA GTCACTCCCT CAATTCCCAT
16201 GTGGCCTTCA GTCTGAGACT AGGGAGATTA AACAGATGCC TGAGAAGCTG
16251 TTATTACAT TTACAAAGCA ACACATTGT CAAAGTGAAGA TAATAAAATT
16301 AGCCCATAAAG GACTCTGGGG GCAAAAGTA AAAATTAAGG CATTAGTCAT
16351 TACAGCAAAT AAGGTTAACCA GGTGTGATGG AGCTCCTTCG GCGTAAGTCA
16401 GCTTAAATTG ACAAGTAAAG AGAGAAATTG ACTGGCTCAC AGATCTGATA
16451 ACTACAGGGCT GGTAGGGCAT AAGCAATATC ATCAGGAAGC CGTGTCTCTC

FIGURE 3F

16501 ATTACCCAAC ACTGGTTGC TGTGCATTCA TTTTATTCCC AGGCATGTTG
16551 TCACCAGGTG TTGGTAATCT GACCCCAGCA ACTCCTGGCT AAATCCACA
16601 GGTTCAGCTC TCACAATAGA AAAGAAAGCA CTTCTTTCT AATGGCACCA
16651 GCAAAACAGG GTCTGCCAAA CTTGGGTTTT GTGCCTGTCT CTGAACCAAT
16701 CACTAGGGTA TAGGGGAGTG CCGTGCTCTG ATGGCCAGCC CTGGGTCTA
16751 TGCCCATTCT TGGGTAGAGG CCGGGTCAGT TCCACCAGAT GAGCATGGTC
16801 TGAGGAAGAA GACGTTGTT TTTCCAGGGG AAAATAGAAG TGCCCCGCT
16851 AGAAGGGAGA ATGGCTGTCA GGAGGGCAA ACGACAGATT CACTAAAATA
16901 GGTGATGCC TAAAGAAAAT AATTTATTTC TAAATTAA GGGAGTATT
16951 CAGTTGTTTT TAATCTTATG GAATTCTACA CTGGGAGGGG GTTGGTGCAG
17001 GAGATTCATG ATATGCAGGC ATAGGCTACA GAATAATGCT TTGAGTTTT
17051 ATCCTTACT TTTCTTCC TTAAGCTTT AAAGACACGA TTCTTCATG
17101 CAGGGTTGCC CTGAGGTGAG CCTCATCATC TCTTTTTT GAGATGGAGT
17151 CTCGCTCTGT CACCCAGGCC AGAGTGCAGT GGTGCAACT TGGCTCACTG
17201 CAACCTCCAC CTCCCAGGT CAAGTGATT TCTTGCCCTA GCTTCCCAG
17251 TGGCTGGGAT TACAGGTGTG CACCACCAAG CCCCACCAAG CCCGGCTAAT
17301 TTTTGTATT TTAGTAGAGA CGGGGTTCA CCGCGTTGGC CAGGCTGGTC
17351 TCAAACCTCT GACCTCAGGT GATCCACCA CCTCGGCCCT CCTGAGTGCT
17401 GGGATCACAA GCATCGCTA CCACGCCGG CCTCATGGTC TCTTATTG
17451 ACCTTTCTA GTCTCTGCTT TCCTGAAGCC AGAGGTCTTC CTATCTCCAG
17501 AAGCTCCAAA GACACACTTT CAAACCCCTC CCAGTCACCT GCCCTTTCT
17551 GATGACTTCT TTCCTTCAAG GTCGCCCTTA GTAACCGATT ATTGAAGAGG
17601 CAAGAGAAAG CCCTCAGCCT TCTCCACTT CACCTCCCTG GGCTCCCCAA
17651 GTTGGCCGA CTCCTCTTT CAAGTTCACA TTTTCTCCTT TCCACAGAGG
17701 TTTGCAACAT TACCTTTAAG AAATCATCTC CAGTCTCTAT CACGTTCAA
17751 CAGTTCTTA CCCCATGCTT TTATCCCTGT CTCCCACCAA TCATATCCAC
17801 CGGCCCTATT GACCGCTTGT GGGAGTTAGA ATTGGAGA CTGGTCATAT
17851 GTCACAAAGT CCTGCTCTAG AAGGCAGAAC ACTCCATTTC CTGCTCCTCC
17901 AAAGCCCTTT ATCTCTCCAG GCCTCTCCTC CTGTAGCTCT GAAGCTGGAT
17951 TGATGAGATT CCCAGAGGGG AGCATTAGT GCTCTGAGTG CTTTGATGAA
18001 ATTGATTAGG TAAATGGAAA CATATTTC GCAACCACCTC TAGCCTGTAG
18051 AAACAATAAG TTGCAATGAT TTGCCATTTC TGAAATAATG AAGGTTCTTT
18101 GTAATTAAAT ATATTCTTT GGCACAAGAG ATTGTTTCC AGCAGTAAAA
18151 TAACCAGAAAT GTTGTATTG AAATGTTGAA AAAATATA CCGTCTGATA
18201 TCTTTAGAGC AGCACTTTCA TTATCAATGA TGGATTTAAC ATTGGTTTA
18251 ATTGTTCTAG CTTCTCTCTT GAAGGGTTTAAACATGCCA ATATTGTGCT
18301 CCTGCATGAC ATAATCCACA CCAAAGAGAC ACTGACATTG GTTTTGAAT
18351 ACATGGTGAG TTGTTCGAGC ATTTCACAC ACTTGAGAAA AATAACCTGG
18401 TACTTGTATA ATGAATCTGT TAATATTTC TGGCATGATA AAACTTTAT
18451 TATAATGTGA AAAGTATCAT GGAAATTTC ATTATTGTGA TTGAGAAC
18501 CTTATTGTT CCACATCCAT CTTGGTCCT GCTTCCTTAC CCATGACTTT
18551 TGCTGTCCCT TTTCCCTCA TCAGCAATAA TAAATGAGGA TCTTGAGTTT
18601 ACCTTCTAAA TAAAACTTT GCACTTATT TTAATCTAAT TTTAATCACT
18651 ATCTGAGCAAG AATCCAACAT TTTTCATTG ACAATAAAGG TAAAATCAC
18701 AAGATATTAA AAAATTGTAT GCAAGCTTGC TAAAGAATAA CTCATGTTGT
18751 ATTGTTGGAA GAAAAAAATAT TTAAATAAGC AGAAAGAACT TATAAGGTAT
18801 GTGTACTTGA CTTGCCCTCA AGGACACTT GAGAGTGGAA AATTCCGCG
18851 TCGTTGTGTT CAGTGCCAGT CATTAAAT GAGCATCTCT GTGCTGAGAA
18901 ACAGGGTTTG TTCTAAGAGC AGCCAGTTAG AAAGACACAC TGTGTTGAC
18951 CTTAACAGTG GGTTCTCAGA AAACCTGGTT ATATTCTTT TGACACCTTAT
19001 TCTTAAATT CTGTACTTCG TGATACCTTC TGACAGTCAA GTCAATGTT
19051 TGCTTTAGGA TGCTATCTAA GCACCACTAA ATTCACTCAC TTCTCTTCT
19101 CCGCTGTTTT ATTAGCACA CAGACCTGGC CCAGTATATG TCTCAGCATC
19151 CAGGAGGGCT TCATCCTCAT AATGTCAGAG TGAGTACGTT AAGGGTCAGG
19201 ACCCTCTCCT GGCTGCCCA CAGAAGGAGA ATTCTGAAAC AGACTGTCTC

FIGURE 3G

19251	ACAAAGCAAA	GTCCTATGAT	ACTAAATAAG	AGGATGGACA	TCACTGATAT
19301	TCCAGAAAAA	AGTTTGTGTT	TGTTTCGTT	TTTGTGTTTTT	TTTAAAAAGG
19351	AAAGAAAAAA	GAAAAGAGT	TGCTGAGTTG	CTTCTTAAGA	TATGGAGCAA
19401	TGTTTCTGA	GCAACCTAAT	GCTGTCAGTC	ATGGCTACAT	GCAAATGTGC
19451	CTTTAGATGA	ATAAACGAGT	GAAGGAGAAAT	TATACTAAAA	GGAAAAAAAGT
19501	AAAGCTAGGC	CATCAAAAAA	TAAATACCTT	CTTCATATCA	GATTACTGTG
19551	GTCTAAGGTG	AAGCTTGCAA	TAACCGTACT	AGCAGATCCT	ATTATATATG
19601	TGGCCCTAAC	TCCCATTTTT	CCAGTCATTA	GAATCAAAAT	AATAAACTCT
19651	TAATTAGCTA	TAATTCTACA	TCTGTTATAA	ATTTTAGAAA	CCATTTATAT
19701	TTCATACTTT	TCATTCCTA	AGGTTTATT	GGCATTAAATT	AATTGATTGG
19751	CTCTTAAAT	AACCGTATGA	AATTGTTATA	TGATGTATTT	ATTCACTTAA
19801	CTAATATTTA	TTTATGTATT	CATTTATTCA	TTCATTTAAG	AAATATTTAT
19851	TGAGTACTTA	TTGCGTAATA	AGTTCTGGGG	TTTCATAAT	GAATAAGTTC
19901	TGTTTCTTAT	TTTCATGAG	CTTAAAGTCC	AGTAAGATAAT	ATGAACCTAA
19951	ATAGGCAGTG	AGGGCCAGTC	TTCAAGCAAC	AGCAATGCAA	GATGGCAGCC
20001	ACCATGGGCT	CAGGCAATT	ATGAAAGCCA	AATATACAGC	CTTAAAATAG
20051	AATGTGGACC	TAATACCCA	GAAGAACTCC	CCTTGTAAAG	ATTGTAACA
20101	AAAATTAAATA	TGAGTAGAGT	TAATAGTTCT	AATGGAATGG	TGAACCCAAG
20151	AGCCATATCA	GCGCTAGCAA	AATGGCAGAA	TTCATATATC	ATCAAAGTTA
20201	TCCTTCAAGA	GCTTCAGCGC	CTAATGATGT	CTAAAGAAAA	TGTGAAACGC
20251	CCTCAGGCCAT	CTGAAGGACA	GTGTTACAGC	AATTGATCAA	AAAGAAAAAC
20301	CACAGGCCCT	TCCCCCTCCC	CCATACTTGA	TGTAAGCAGT	CTTCATTTTC
20351	CATAGTAGTA	AATTTCTAG	ATACAGCTTG	TAGAGCTAA	AGTACTGGAA
20401	AGAAAGCTCC	CATTCAAAGG	AAATTTATCT	TAAGATACTG	TAAATGATAC
20451	TAATTTTGT	ACATTGGAA	TATATAAGTT	GTTAGCCTGG	CGCGGTGGCT
20501	CACGCCCTGTA	ATCCCAGCCC	TTTGGGAGGC	CAGAGTGGGC	AGATCATGAG
20551	GTCAGGAGTT	TGAGACCAGC	CTAGCCAACA	TGGTAAACCC	CCGTCTCTAC
20601	TAAAGATACA	AAAAATTAGC	CAGGTGTGGT	GGCGCACACC	TGTAACCCCCA
20651	GCTGCTCGAG	AGAGTGAGGC	AGGAGAATTG	CTTGAACCCA	GGAGGGAGAG
20701	GTGCAGCGAG	CAAAGATCAC	ACCAATGCAC	TGTAGCCTGG	ATGACAGGGC
20751	AAGACTCCAA	CTCAAAAAAA	AAAAAAA	AGAAATATGT	AAGTTGTGCT
20801	ATAACAAATA	AATAGGCAGT	GAGAACAAA	GTGCTAAAGC	CTATGACCAT
20851	GGTAACCTAGG	AATACTGTGG	GAACACATAA	TAAGGGAAAC	TAACCCAGTC
20901	CTGGAAGTAA	GGTTTGGAA	AGGAATGTTT	GAGGACAAAG	GGTTAAAGAG
20951	AGTAAAAAAA	AAAATTAAAA	TACCAGTTA	GCTGTGTGGA	GAATGGGATA
21001	GGGAGCTAAC	TAGAGAAATC	AAATAGGAAT	GTTTCATGGT	ATGTTAAGGA
21051	CCTGGTAAG	GGTGAAGACC	ATTACATTAT	CTGCACCATC	GCGGGACTTT
21101	TTTTTATGG	TAATGCTTGG	CAATTAAAT	AGAGGAGCAG	AGAATGTAGA
21151	CAGTTGGATT	GAGTCAGGT	TGAAGTTCTG	CCAGACATGT	GAAAGGAAGA
21201	GACAGGTAGG	CAAGAGAGTT	GAAGAGATTA	TCAAGACAGA	AGTTAATGTG
21251	CTGGCCAGTG	GCATCTAGTC	TGAGTCTAAT	CTGAGGGAAAG	GAAGTGAAGA
21301	TAAGCAGCTT	GCTGATAGTT	ATGAAGAGAG	TGGAAGGCTT	CAAGGACCTA
21351	CAGGTGTTGA	TTAAATAGAA	GAATGATTGG	AGAAAGAATA	ACTGTGAGAG
21401	AGTGAGATT	TCAGGCTTGA	GTGACTCTCA	CATACCAAGAC	ACTGTGCTAA
21451	ATGCTTCAAA	GACATGATCC	CTGCCCTCAA	GGGACTTACA	GCCAAAAACAA
21501	AGAGATAAGA	AATACACACC	AATACTATTA	TAGGACACTT	GTGTAGAATA
21551	TCAAGAAAGA	AATACGATCT	AGTACTGTAG	ATGTGCAACG	GCATCAAAGA
21601	TATCTTCTAG	TTTCAAGAAG	TTTCAGATCG	GCCGGGCGCG	GTGGCTCACG
21651	CCTGTAATCC	CAGCACTTTG	GGAGGGCGAG	GCAGGGTGGAT	CACAAGGTCA
21701	GGAGATCAAG	ACCATCCTGG	TTAACACGGT	GAAACCCCGT	CTCTACAAAA
21751	AATATAAAAA	ATTAGCCAGG	CGTGGTGGCG	GGCGCCTGTA	GTCCCAGCTA
21801	CTCAGGAGGC	TGAGGCAGGA	GAATGGCGTG	AACCCGGGAG	GTAGAGTTG
21851	CGTGAGCCGA	GATCGCGCCA	CTGCGCTCCA	GCCTGGGCGA	CAGAGTGAGA
21901	CTGCGTCTCA	AAAAAAAAAA	AAAAAAA	AAAGTTTCAG	ATCTTAAACA
21951	CACTGCATT	CAACAGTCTA	GAATAGGAGA	GCATGTTACA	GGGAGAGAAA

FIGURE 3H

22001 ATGTTTCAG CAAAGGTACA GAGTAGGGAA ATAGAGGATA TGTTCAAGGA
22051 AGAGGCCCC AGAGTCATGG TTTGTTAGGG TTAGAGGAAA CACAGTGT
22101 TCGAATCTCC AGGTTCCATT AGTGCCTTAT GAAATCAATA TGGTGGTTAG
22151 CAACCTGCAT TTTAAAAAAAT GAAATAAAATG GATGAGAAGA GAATAGAAAA
22201 TATTAGCATG CATTACATT TGAAAGAGCA AGTATTATTT TCTGCAACTT
22251 TTGCTCCAAT TGTAACGTGA CTTATATTT TATGTATGGA TGTGAATACC
22301 AGATACATAT ATATTTCTTA CTGTAGACTG CAGTCAAAAA ATCTTTAAAG
22351 CACTGGCCTG GTCTAACTTC CTTATTTGC AGAGGAGAAA TCCAAGATCT
22401 GAGAGGACAA ACATTTGCC TGAGGTTATA GAACCAGCTT ATGCCATTGC
22451 TAAAAGTGT TCTTAGTTAA AATTCTTCC CACTAGTGCC ATACTGCACT
22501 TCTAGTTCTG TTGGCCTGAA ATACAGAATA TATTAGTGAA ACAGCATACA
22551 CAAGTCTGGG GAAATATATT GGGTAGGTGG CTGAGAGCCT CATTCTAA
22601 GAAATGTGGA CCTTAGGCAG GGTATGGTGG CTCACACCTA TAATTCCAGC
22651 ACTTTGGGAG GCCAAGTCAA GAAGATCGCT TGAACCCAAG AGTTCAAGAC
22701 TAGCATGGGC AACATAGCAA GACCTCATCT CTACAAAAAA TTTAAAAATC
22751 AGCTGAGCAT GGTGGCATAAC GCCTGTAGTC CCACCTACCT GGGAGCTAG
22801 GTGGGTGGAT CGCTTGACAC AGGAGTTGA GGCTAAGGTG AGCCATGATC
22851 ACACAACTGC ACTCAGCTT GAGTACAGA GGAAGACCCCT GTCCCTAAA
22901 AAGAAAGAAA TGTGGATTT ATTCCCTAGA CAGTACAGTC ATTAGTCATT
22951 AAGTTTGAGT TGAGAGAAAA TAATATGATC AGAAGAAATT TATATCACTG
23001 TGGTCTGTAG GATATATGAA AGGAAATAAG AGACTAGAGT CAGGGATTCC
23051 ACTTAAGTGT TTGTTTGT
23101 AGGCTAGAGT GCAATGGTGC AGTCATGGCT CACCGCAGCC TCAAACCTCCC
23151 AGCCTAAAT TATCTTCCCA GCTCGGCCTC CCAAAGTGT GGAATTACAG
23201 GTGTGAGCCA AAGGGTTTAT TGATGTGGT
23251 TTCAGTGAGC AGACAAGTGA CCGGGAACCT GACTCAACAA GTCTGGTT
23301 AAGCCTGAGC CTCTGCATT
23351 TGGTCAAGAG CCAAGCACTG AGCAGCAAGG ATCTAGTTAG CAATTAGTA
23401 TCAAGGTTGA TATTATGGTA GTGACAATAA GAATGGAGAG GAATGTAAA
23451 ATCAGTAACA AAGAAGAGTT CACCTCTTGG TAATGTGAGC ATGAGGAGGG
23501 AAAGGATGGG GCCAACATA ACTGGTTTG TGTTTGACTG ACGAGGAGAA
23551 TTGTTAGCTCT ATTAACAGAA ATAGGAGAAG AAGTTGGTT GGAGAGAAAG
23601 AGGAGTCCTG TTTCAGACGT GTTGAGGTCC CAGGTGAGAC AGGATCTCCA
23651 AAGGGAAATG AGCAGTAGGC AACCTAAAAG GAAATCTGTG CTCAGAAGGG
23701 AGCTGTGAGC TCGACGTGTA GATCTGAGGG TCATCAGCAC ATAGAGTTA
23751 GAAGACAAGG AGTAGGCAAC CAAAAGAGCA AATACACAAA GAGAGGAGGA
23801 CTGATGATGTA GACTTTGCC TTTAGGATG AGAAGAGGAA CAGGAAATGA
23851 AGGAATGAAG GGAAGCAGCT TGTAGGAATG TAGAGCATCT GAAAAAAAGAA
23901 TACACACTGT CATGGAAGTC AAGGGAAAGA GAATTTCAAG AAGGAGGGTA
23951 TGGTGGACAG TATTACAAGC ATCAGGAATA CAGCTAAAAG TCATACTCTT
24001 GACTGCATTG ACCTTGTGGA TTTGTGAGGG ACACACTAAT AAATAAAGGA
24051 ATTATTTGTG GGTATATGGA GGCACAAAGG AAGAGGTTAT CCAAATCAA
24101 GCAGGTGGGA GTAGGGATGA GTTCTCCAAG GTGGAGGCAT CAGTGAATGT
24151 GGGAAAGGGGC ACAGAGCATC CATGCCCATC CCAGGCAAGC CACCCTCCAG
24201 AAGCCTCCAT GAGAGTTCAAG CTATCCAGAA GGTCTCTGTA CCCTAATCTT
24251 TCTGGGTTTT GCATAGGCTT CATTGTGTAG GCATGATTTA TTAAACTATT
24301 GCCCACTGGT GATCAAACCA ACCTTCAACC CCTCTCCCT CCCTAATCAT
24351 GCCTTGGTCT TTCCAGTGC CAGTCCCTAT CCTAAGCTAC CCAATGGTCT
24401 GCCAGCTATC AGTCAAACCT ACAAAAAGAC ATCACTTTGG AGATTCTAAG
24451 GATTTTAGGA GTTGGCTGTC AGGAATTAG TTGAAGATCA AATATATATT
24501 TCACAATATC ACAGTCGTGC TATTTTATAT CAGGCGCCAT TAAATGGTTT
24551 TAAACAAAGA GGTGATAAAAT TCAGATTTT CTTTTATAAA GCTTACACTG
24601 ATGACAGTGT GGTGAATAGA TTGGGATGAG GGAATAACTT TTTTTTGAA
24651 ATGTTATATT CCCCTGACCC TACTTTCTCC TTGTTTTCTT CTACCTCTCT
24701 CCCCCCTACTC ACACAGAAAA CTTCTCTCCC TCTACTCATT CCCTGAATGC

FIGURE 3I

24751 TGGTGTCTGT TAAGGTTCCA GCCTTGACAG TGAGGGCTAAT CAGAACCA
24801 GTGGTACAGA TGTGAGATGA TGGTGGGAGA AAGTGGACAG ATATGAGACC
24851 ATTACTTAG CCGGAACCTGA CGGGAAAAAC AAGAGTCAGC GATATTTTT
24901 TCTGGATCTG AGTATTAAAA TGGATGATGG TGCCATTCA C TGTGATAGAG
24951 AATCAGAAAG AAAAATTAT TTTGGAGAGA TACCATGAAT TGTGTTTAG
25001 ACATGCTAAG TTTGAGGTGA TTATGGGATG TACAGGCCAG CTCCAGACTG
25051 TGTGGGCCTA AAGTAGAAAG GCAATCTGAG TTGGAGATAA AGATTTGAA
25101 ATCATCAGAA TACGGTTGTT CATTAGAGCA CTGTCAGTGG GTAAGATAGC
25151 TAAGGGAGCA TGTGTAGAGT GATAACAGAA GATCAAAGAC GGAACCCCTAA
25201 GAATAACAAT ATGTTATTAT TTATTATTT ATTATGTTT ATTTTTTAAT
25251 TTTATTTTA TTTATTATT TATTTTAAAGA CGGGAGTC C GCTCTGCTGC
25301 CCAGGCTGGA GTGCAGTGGC GCAAACTCAG CTCACTGCAA CCTCCGCTTC
25351 CTGGGTTCAA GGGAGCCTCC TGCCCTAGCC TCTCAAGTAG CTGGGACTAC
25401 AGGCACCCAC CACCTCACCT GACTAATTT TGTATTTTA GTAGAGACGG
25451 GGTTCACCA TGTTGGCCAG GCTGGCTTG AACTCTGAC CTTGAGTGAT
25501 TCACCTGCCT TGGCCTTCCA AAGTGTGGG ATTACAGGTA TGAGCCACTG
25551 TGCCCTGGCCT ATTTTTGTTT TTTATAGAGA TGGGGTCTTG CTATGTTGCC
25601 CAGGCTGGTC TCGAACTCCT GGACTCAAGC ATCCTCTG CCTTGGCCTC
25651 TCAAAGTTCT GGGATTACAC ATGTGAGTCC CTGCGCCTGG CCAGAATATC
25701 AATATATTAG ATTTTAGTAG AAGTAGAAC TATGAAAAGA ACAGCCAGAG
25751 GGGCAGAAGA AAAATTAGGA GATTGTGGAA CAAAAGAAAG AGAGTGCCTC
25801 AGGAAGGAAG GCATGGTCTA TGATGCCAA TGCTGCAAAG ATAAGGAATA
25851 AGAAGTATCC ATTGGGTTTC ATAGGAAAAG TCATGGGAA CCATGGTAA
25901 AAAACATTGT GAATGACACA ATCGTTGCAA AAGCATTTTT ATAGGGGGAT
25951 GAATTITGTA TTTCAGAGGA CAAACAGTTC CATACAATGG CAAGATCTAG
26001 TGTGTGACCA CGGGAGTTAG TGTCTGAAGT GGATTGGAGA AGCAGATCAT
26051 TGGAGCTGAG GTTGGCTAGA GCTGTTCTCA TGGACACTAA TGTCACTGGAG
26101 TCAACAGCTG TGATCCAAGT GCCCACATCT TCAGTGAATG ACAGAGAGGG
26151 ATTGAGAGTT CAGTGAATGA CCGCTAAAAG AAGAGTAATG GAAGATGTGG
26201 CTGGATGGCA TAAAATCCA AGGGACAGGG GTTTTACTT AAAAGTAGAG
26251 AAGTAATGGT TTTGAAGTGG TAGTGGGAA AAGGGAGGCA GCTTATGACA
26301 CTTGTCAGTG GTCAAAGGTA TGAGGAAGTT ATAGAAAAC TAACATCCAC
26351 TTGAGAATAT TATAGGGAAG CAGTGAGCTC AAGGTCTCAT TTAAGGAAAG
26401 GAGCCAAAAG GAAATTCAAG AGAGGTTAGC TTTTAGGTAG TTTTTAAAGC
26451 AGGATTGAAG AATGGGAGACT AAACAGTGA AATGTTGGG AGAGAGAGGA
26501 GCAATAGATA TGAGGCTAAA CAGAGGAAGC ACAGAACAGA ATGGAGATGA
26551 GTATGTTGGG AGGAAAAGGA ATAGTCAGAG GCTTATATT TGAGTTGTGA
26601 CCAAGGAAGA CAGGGTGGGA ATCCTCGTGA GTTATCTTG TTTCAGATT
26651 CTAGTAGAAT GAGTCCCAGG GATTCCAGGG GGGATGGAAG GACTCAGGCT
26701 TCCCTATAAG GAGTTGGCTA ACGGATCTCA TTGGTTTTG AGTAACCTCCT
26751 GCCCCAGATG GCACTAGTTC AATGGAATTAA TTTTGTCCC CAAAACCTTA
26801 TTGAGTTGGA AACAGGTCTA ACTCCTGGGA TCTGGGAAGC CTTTCTGGAA
26851 AGAGTCACCC ACGATCTGGC TGATGTTGAA CTGTGCAGAC ACCATCATAT
26901 TTGGTTATGT TAGGATGCAA TAATTGGTA AGCTTCTGTA GTGTTGAATG
26951 AAGAATCCAG GTTGAAGGG ATGAAAGGGT GAGTGGGTGA TGAGGTTTGT
27001 CAGCACAGAC TGCAATTTC AGAAATGTGG TTATAAAATA CCATACCTTA
27051 ATACCGCAGT GCTTTACCAC TCACAAATGC CTGTAGACGT ATCTGGCAGA
27101 GAGGAAAGGG GTTGAATGGC AAGAATGTGG GAAGGGACTG TGGCTAGTTA
27151 GTAAAATAG TCTACACTTG GGACATAAAA GGCATTTCAA GCTGACCTAC
27201 TAAGAAGCTC TGTCTCTGAC TCAGCCAGCT GGCTCTCTCC TCCCCTGTCA
27251 TGTGTTCTT CATTGAGGCC TGGTTTCTC TGTAAACTGA GGATAAGCAT
27301 TCAGACAAGT CTGAATTGTA GTCTGGCTC TGACTATTCC TAGACATGTT
27351 TAAAGGTTA CATTGAGGCC TGGTTTCTC TGTAAACTGA GGATAAGCAT
27401 GCTATCCAA AGGTTGTATC CCTCACTGGT CACCAAGCTTC CTGTCTCTA
27451 TCCACCTGTC TTCCTCTTCC TCTTCCCTA GTCCCTGCATA TTGAAAAACA

FIGURE 3J

27501 TTTTTTTTTT TTTTTGAGAT GGAGTCTTGC TCTGCCACCC AGGCTGGAGT
27551 GCAGAGGCAC GATCCTGGCT CACTGCAACC TCTGCCTTCC AGGTTCAAGC
27601 AATTCTCCTG CCTCAGCCTC CCGAGTAGCT GGGATTATAA GCATATACCA
27651 CCACATCTGG CTAATTTTG TATTTTTAGT AGAGATGGAG TTTCACCA
27701 TTGGCCAGGC TGGTCTCGAA CTCCGTACCT CAGGTGATCG GCTCGCTTTG
27751 GCCTTCAAAA GTGCTGGAT TATAGGCGTG GGCCACTGCG CCAGTCTGAA
27801 AACACGTATTT TTAAGCACAT ACTATCGTAT CTTCTTGTCT TTTACCTGGA
27851 ATTTAAGCTG GTTGTGGTAA TTACCTTTTC CATGGACATT TATATTTATA
27901 ACCAACATAGA AGGTTTAAAT GTCAGTGTAG GAATTTGTG CTATGGAAGC
27951 TTCGTGGCTT GGTGAATGGT AAAATGAATA ATGTGTGTAT ATTTGAAGCA
28001 TCAGAAAGAG AAAATGCTGG GAAGATTCTAT AGAACCGAGT AACATTTGAA
28051 CTAGGAGTCAT TAAGAAATT TAAACATTCT TAAATGGTTT ATGAACCTGA
28101 TGTTGTTAGCT ACATGAAACC TGATAGCTG CAGGTATGCT ATGGTAGGTA
28151 AACTCTCCAT GCTCTGCTT CCATTGGACC ATTTGGCTCC AATGTCTCCA
28201 GGTCTTTGTT AGATCAATAC TGGTCCTAGC ATCTCTGAAA GTCCTAGCTT
28251 TCTAAGATGC TGTTGAAAAA GAGGATTAAT CCACATAACT CTGCATCTGC
28301 CATTGGGCC ATGTCCTCAGG AATGCTGGC CTAGCCCTC CTTCTGAAC
28351 TGCCAGAACCA CGTTCTCAGT TGACATACGT CTTGTAAAT ACTGATGTTG
28401 GTGTTTGAAT TCTCAATTGC CAATGGCACT GAAAATAGC AAAAGATACT
28451 TGAATACTA AGCATTCTT TTTTCCCAGT AGTTTCTGTA GTGATGGAA
28501 CCTAGTAATG GCTTTGGTTT CTGTGCCTCA TAACCACATG AAACATTTTT
28551 AATTTGGGGC TCAGAATGTG TTTTCCCTT TTATTTCTCC ACCACTACCA
28601 TTTACCCCTTT CTCCTTCTT CCTCCTACAA TTTGTTCTT ATTCTTTTTT
28651 GATTTTTTTT GAGGGGGGGGG GGTCTAACCT ATTGGTCTCT CTCTTCCCTT
28701 TTCATCTGTA CTGTGTATTT CCCTGTTT CAACCTTGAA TTTAAGACTT
28751 TAAAAAATAGC TTTAAAAAGA TAAAGATTC TTTATTTCTT AATACCATCT
28801 AAAGATATAT TTTTTAGTGT GGTCTCTTG TGTTGTGTTT TTTAAAGGGT
28851 TTCATATTGG AGAGCCTGGA AAACCTAACG AGTTGTAAAC TTTAGAATAT
28901 CATTCCAGG TCAACTTGA TCTTATATGC CAAGTTCATC GGTGGGGAAA
28951 AAAATTAAAT CTTCACACATC TAAATCAATA ACTAGTGTTC CAAAGGAAAC
29001 TTCAAAGTTT CACTTAGAT TTTTAAAGAA GGGTAATTCC TTCAGTATCA
29051 AAGAAATGAG ATGTCAGGAA AAGCCAGAAT CCCTTGTGTT AGGACACAGT
29101 CTAGTTACTT GACTTTCTT GTCCTTTTC TTCCCCCTCT GAATGTAAAA
29151 ATCTTCTTCT TCTTCTTTTT TTTTTTTTT TTGGTCTCTC AAGAGACACT
29201 TTACTATAT TCTTTGAGAT GACTGTTTTT GATTAGAGG CGAAATCAGC
29251 ACGTGGTGGC TCAAATCTCC TTATGGATAG TGTTCTTCC TTCCAGCTTT
29301 TCATGTTCA ACTTTGCGG GGCCTGGCGT ACATCCACCA CCAACACGTT
29351 CTTCACAGGG ACCTGAAACC TCAGAACTT CTCATCAGTC ACCTGGGAGA
29401 GCTCAAACGT GCTGATTTTG GTAAGTCGCC CCTCGGGTCT CATTCTGGGC
29451 TGTGAACAAT GATGCTTTG TGTGCACTTG TTTAAGCGTT GACTGGCCT
29501 GGCCTTTGAA AACTGGAGGC CCAAGAACAT GATGCTTTGT GAGGATATCA
29551 AACTACCACA AAGGAAGTGT GAGGCACGAA ACAGGGAGGG ATTGGTAGCT
29601 TTCTAGGATT CCACCAAGTC CCAGTTAGT CAGATGGCCA AAAGCTGGGC
29651 ACCCTTGCTG CCCACTGCG AGTTTGATA TAGAGACATT GGTAGAGTAA
29701 ACTGTACTT A GTAAAGTTTC CTAATCTAA GTGAATATAC AAATTATATT
29751 GGAATAGATT GAGATTATCC CAAGATGATA AAGAGGTTAA CCCCAGATTG
29801 TAGCATGGAC TCCTGTCAGG ATGGAGACTC CAGGACACTT GTTCCTGCTC
29851 TCCTACCTTC TTTATATAAG TGTGAGATGC AAAGTTTTAT TCCCATTAAA
29901 GTGAAGCAGA TTTCCTCTAA GTATCACTGT ATCCTTCCAT TTTAGCACTT
29951 ATCGCAGTTT ATAATTATAT TCACACACAT AAATACATAC ATGCATACAT
30001 ACAAAATATAT ATACATGTGT GAGCACACCC CCACACACAA ATATATATAG
30051 ATTTGCGTGA TGATTTGTCA TCAACTGGAC TGTAAGCATA ATGAGGGCAG
30101 CCTGGGTTTG TTTTGCTTA TCATTTTATC CTTAGTGCCT GGTACCATAG
30151 TAGGTGCTTA ATAAGTACTT GTTGAACAC CAGGCTCTATG TGAGCTAAGG
30201 ACCACTCTT CTCTGTTGG CAGATGCCA ATGGTGATAC TATCACTGCA

FIGURE 3K

30251 GTATTTATTG TGAGATGGCA GCTTTATCC TGACATGTA GCATTTAAC
30301 GATATTTGTT TATCAATTCT CCACAATAGC AAACTCATCT ATTGAAGTTT
30351 TTCCCAACAA TAGATCATGC AATTCTGTGA GATAAACAGC TGACTGACAG
30401 AAAGACTCAT TTTGCAGAAC AGTACTTAGA AATTCATCTA AGGTCCCTACC
30451 AAACTAATTA ATTTGGATGA GCAGTCCCTA CCGTTTATCT ACTAAACTGG
30501 GCTTTCTGG AGTGCCAAA CGGAAGGTGG CCATGTTAGT CATGAACAGC
30551 TCAGTTCTG TTACAGAGAC CAAAATTAC AGAGGTATAA CATGCTAGAA
30601 ACTTAACCTT CTTTCGCATC ACAGTCCCTA CCTAAGCAGG CAGAGCATGT
30651 ATGGTGGCCC CATGCTATCT TGCCCCAGGC TGCTCTGTC ACGTGGCTCC
30701 TCCATCCCCA ATTGTATGTT TCAAGATGGC TGCCACTTCC TGCTCATCAC
30751 AGCCCAGAGG AGGGAGAAAA GAGAACAGA ACCCTTAACC CCTCCACTAA
30801 GGCTATAATCT GGAAGTTCAC ACATCACCTC TGTTCATATC ATATAGGCAA
30851 GAACTTAGTC ACCTGACCAC ACCCAGCTGC CAAGAACGCC ACATCTAGCT
30901 GCAAAGCAGG CAAAATTG AGAAATTAC TTGATGAAGT GATAGACAAG
30951 AGTCAAGATA GTGATTAGTT CTACTAAAAG CACCTAAAGT TTGTGTGTTA
31001 TTTTTCTAA TGGTGTCTAC CCTGGTCCAG TGCTCATGG TGCAAGCCAA
31051 GGTCCAGAAC GATGGGTTTT ATGCTTTCC CTTTGGACA GGTCTTGCCC
31101 GGGCCAAGTC CATTCCCAGC CAGACATACT CTTCAGAAGT CGTGACCCCTC
31151 TGGTACCGGC CCCCTGATGC TTTGCTGGGA GCCACTGAAT ATTCCTCTGA
31201 GCTGGACATA TGGTAAGAGT GGTGCCGAGA AAATGTGAGT CATCCTACTC
31251 ACGAGGGTTG CTTTATCATC TACATTATAT TTTAATAATA ATTCTAAAAA
31301 TGGCAATCAC GTATATATT TTATATATAT TTATATTTT ATATTTATA
31351 TATATTTATA TAGTTATATA TTATATTTT ATATATTTT ATATTTATA
31401 ATATTTGTAT ATATTTATAT TTATATATAT TTATATATAT TTATATATTT
31451 TATATTTTTA TATTTTTATA TATTTATATA TATTTATATA ATATTTATAT
31501 ATATATTATA TATTTTATA TTATATATA TTATATATATT TATATATATT
31551 TATATTTTTA TATATATTAT ATATTTATA TATTTATATA TTATATATAT
31601 TTTATATATT TATATTTTA TATATTATAT ATATTTTTT ATATATATAT
31651 ATATGTATT TTCTTTTTG AGATGGAGTC TCACTCTATT GCCCAGGCTG
31701 GAGTGCAGTG GCACGATCTC AGCTCACTGC AACCTCCACC TCCCAGATT
31751 AAGCAATTCT CCTGCCTCAG CCTTCTGAGT AGCTCTACTA AAAAATACT
31801 AATATTTGTA GAAGATTCTT GCAATTATTC TATAACCTTT TACTGTTGAA
31851 CTGAGACCCA CAGAGTTCTT GCCCAAGGCA TCTTCTGAAT CTGACACTCT
31901 TTTTATGTTA TTTTATTTTT TGAGATTGGG GTCTGCTAT ATTGTCCAGG
31951 CTGGTCTTGA GCTCCCAGGC TGAAGCAGTT CTCCCACTTC AGCCTCTTGA
32001 GTAGCTGGGA CTATAGGGCT GCACCACTGC ACCCTGGCAA TCTCATGCTC
32051 TTTCTTCAC GCCTTTCTC CTAGCTCCTC TCTTTAATCC TTTGCCCTGT
32101 CTTCTCCTTG ACACCTTATC CACAGAGAAA CAAACATATA TCCCCAAACC
32151 ACAGACACAC AGATGTGTGT GCACGTGCAT GTGCATGCAC ACACATCTGC
32201 ATGAACATAC TCACACATGT CCAAACGTAG TTCAGAGCCT GGTTTAGGAA
32251 AAAAAAAAAAA AAGCATAAAG ACCAAGCTTC AAGACACCTG ATTTTCATGC
32301 CAGTCGATT TCTAATCAAT TAACTCTGGA TTCTGTTATC TTGAAAAAGT
32351 CATGTATCCT CTCTGTGTCT ATGTTTCTCC ATTTTTAAAA ATGAAGGTAA
32401 TAAACTCTCT CCATCTGAGT TAAATGGAAT TGTAGTACAA ATATAAGAAC
32451 CAAATAGGTG GCTGGGCTTG CCGTCTCATG CCTGTAATCA CAGCGCTTTG
32501 GGAGACCAAG GCTGGAGGAT CGATTGCTTC AGCCCAGTTG TTTAAGATCA
32551 GCCTGGGTAG CACAGTGAGA TGCTGTCTCT ACATTTTTA AAAAATATTAG
32601 TCAGGCGTGA TGGCTAATTA AACACTTCAG GAGGCTGAAG TAGGAGGATC
32651 TCCTGAGCCT GAGAAATTGA GGCTGCAGTG AGTTTTGATG GTACCCCTGC
32701 AATCCAGCCT GGGTTACAGA GCGAGACCCC GTCTGAAAGA AAGAAAGAAA
32751 CAGAGAGAGA GAGAGAGAGA GAGAGAGAAA GAAAGGAAAA GAGAAGGAGA
32801 GGGGAGAGGG GGAGAAAGGG AGAGGGGGAG AGAGGGGGAG AAGGGGAGAG
32851 GGGGGAGAGG TGGGGAGGG A GGGAGGGAGG GAGGAAGGGA AGGAAGGAAG
32901 GAAAGGAAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA GGAAGGAAGG
32951 AAGGAAGGAA GGAAGGAAAG AAGGAAAGAA TCCAGATAGG TGCTATCAAG

FIGURE 3L

33001	TAAAGCCACA	GAGTTGGGGA	GGCTCTAAGG	TTAATGGGTT	ACAATAGTGA
33051	GCATGGGCTG	TCAGACATGC	ATCATCCTAG	AACGGCAGTG	TTATTTCTC
33101	TGGATCATGT	TCCTGGAGAC	TTCCCAGTCA	TTTGGGGGCC	ACTGTTAGAT
33151	ATGTGATGAC	TTTACAGACG	TAGACAACTC	CCCAAAGGTA	AGGAAATATA
33201	TGAATCTCTT	TCAGTACCTT	GGAAGAAAGG	TTTATATAA	AAACACAAAG
33251	CCCCATTTTC	AAAAATCCAT	AATTGATTTT	AAAAAATTAA	ATGGTGTCCCT
33301	AAAAGGCTAA	ACTAAGCTTT	TAGATCTCCC	AAAGAATTAA	GAAAGGTTGC
33351	AGACATTTTT	CTCCAGTGT	GAGTCATTGA	TTTCTGATAC	CCAGTACAAT
33401	TTATAGAAAT	ATCATCTGCT	AGTCAAAACC	CTCCTGAAAC	TGTCAGCTCA
33451	CACCGCTCAG	CACTGTCACT	TCAAAGGACT	CCGGCAGGCT	CTGGCTTACT
33501	CAGCTCTTAA	TGATGTCTTC	CTGATTATGT	TTCACAGAGT	GAAACTTCTA
33551	CCCGTCAATT	TTAAACTAAT	TTTATTATGG	AATAGTTAAA	ACATTCAAGA
33601	GTATATATAA	CATATATGTA	GATCAGTGT	TCTCAACCCAG	GGAGCAATT
33651	TGCTCTGCAG	GGGACATTG	GCAATGTCG	GAAACATT	TTGTTTCAC
33701	AGCTGGGGGT	GGGGTGGTGG	GGGGTATCAC	TGGCATCTAG	TGGGTAGAGA
33751	CCAGGGATAC	TGCTAACAT	CCTACAGTGC	AGAGGACAGC	CCCTGCAACA
33801	AAGATTTTC	CAACCCAAA	CATCTGTAGT	ATCAAGATTA	AGAAAGCCGA
33851	TGTAGGTTAA	GAAGCTTAAT	TTACTTTAG	AGACAGGTC	TCCCTGGTT
33901	GCCCAGGCTG	GAGTACAGAG	GTGAGATTGT	CTCACTGCAG	CCTCCAACTC
33951	CTGGGTTAA	GTGATCCTCC	TGCCTCAGCC	TCCTGAGTAG	CTGGGAATAC
34001	AGGTGTGTGC	CACCAACCT	GGCTAATTAA	AAAAAA	GTGTAGAGAC
34051	AGAGTCTCAC	TTTGGTGC	ATGCTGGTCT	CAAACCTCTG	GCTTCAAGAG
34101	ATCCTCCTGC	CTTGGCCTTC	CCAAGTCTG	GGATTACAGG	TATAAGCCAC
34151	CGTCCCCAAC	CAATTAAGAA	GCTTAATAAC	GTGAACCTCA	TAACCTGCTA
34201	CCCAAGTGTAA	CAACTAGAAC	ATAATCCGTA	CTGTCCTATC	AACTGTGTCC
34251	CTTCCCAC	AACCTGCC	TCCACTAGAA	GGCCTTCTAC	CAAAATT
34301	TTTCTTTT	TCATCAGTAT	TCTCATATCT	TTTAA	AATCCTTTA
34351	CATTTAGAG	GTATTCTAA	AAATATT	TTGTTTACT	TGATTTAAG
34401	GGTTGTTT	TTTGAGACG	GAGTCTCGCT	CGTCGCCAG	GCTGGAGTGC
34451	AGTGGTGC	TCTCAGCTCA	CTGCAAGCTC	CGCCTCCAG	GTTCACGCCA
34501	TTCTCCTGCC	TCAGCCATGA	TGTTATATTG	CTTCTAGTCT	TCTGTGACTT
34551	GGTTTGT	CATTCAATAT	GTTACATGTT	TCTAAGATTC	ATCCATGTT
34601	ATCTGTTAG	CTATACTTTA	TTTCTGTTA	GTGAATATT	CATTTT
34651	AATGTCTATA	GCTTTGCAAT	AATACTTGT	ACCTTGTAGG	CCAAGTCTCC
34701	CAGCCTATT	ATCTTCTTCA	TGAGGATACA	TCAGATAAAC	CTAGTTAAG
34751	GGACATTCTA	CAGAGTAAC	GACCTGTACT	TATTGGAAGT	GTCAAGATT
34801	TAAAAGATAA	AGACTGAGGA	ACTGTTCCAG	ATTAAGGAG	ACTCCAGAAA
34851	CCTGCCAACT	AAATGTAACG	CATGGTCTA	GATTGGATCT	TGGGGGAGAT
34901	GGTGCTCTAA	AGAATACTGT	AGGGACTATA	GGTGAAATT	CAGTAGGGAC
34951	TGTGGATTAG	ATAGGGGTAT	TGGATGAATG	TTAAATT	TGATTTGAT
35001	AATTGCACTG	TTGTTATGTA	AGAGGATACT	TTGGTCTCA	AAAAATACCA
35051	ACATAATTAT	TTAGGGATGA	AGAGTCATGA	TATCTACAAT	TTACTCCCTA
35101	ATGTTTCAGA	AAAGATATAG	ACAGACAGAC	AGACAGACAG	ACAGACAGAT
35151	AGATAGATAA	AATAACGAA	CAAAGTGC	AAAATATTG	CGATGGATGA
35201	ACCTGTTGG	AGGATATAAG	AGAGTTCTT	ATACTGCTGC	AACTTTCTA
35251	TAAGTTGAA	ATTATTCAA	GATTAAAAGT	TGCCTCCAA	TTGCGAAATC
35301	CTTGCTGTT	CATCAAAGTT	AGTGTAAAGAC	AGCACTAGCC	TAATATGTGA
35351	TCAGTGT	TAATTCTTC	ATGTGTGTT	GAGAAGAATG	TGTGTGTCCA
35401	CCCAATGTT	GAGTGTGCT	GGGGTTTTT	TTTGT	GTTTTGTT
35451	TTGTTT	TGAGACAGAG	TCTCACTCTG	TCTCCATGCC	TGGAATGCAG
35501	TGACTCAACC	TCGGCTCACT	GCAACCTCCA	CCTCCTGGGT	TCAAGCGATT
35551	CTCCGTGCC	AACCTCCAA	GTAGCTGGGA	TTACAGGAGC	ACACCATCAC
35601	ACCCGGCTAA	TTTTGTAGT	TTTAGTAGAG	ACGGAGTTTC	GCCATGTTGG
35651	CCAGGCTGGT	TTCGAACTTT	AGATGTCAAGG	TGATCAGCCT	CCCAAAGTGT
35701	TGGGATTACA	GGCATGAGCC	ACCGCGCCTG	GCCAAGTACC	CATTTTACA

FIGURE 3M

35751 TATGTTCAAA AATTCAAGGT TGCTAATTAT ATTATCCAAA TCTTCTTTAT
35801 ATTATTTTTG TCTTTTTAAC CTACCAATGA AAGGTGTGTT GAACTCATT
35851 ACTATATTGT TGATTGTCA GAATTCTATC CACTTTGCT TTATATGCTT
35901 TGAAGCTATT TTCACTAAGG GCAAATAAAAT TTAAGACTGC TCATTATTCC
35951 TTTGTACACT TTAGTTACCA CTTTCAGAAT AATTTTCAATT TCTCCTGAAA
36001 TACATCTTT AGAGTGTGTT GTTTGTTTG TGTGTGTGTA GGCCTGCTGG
36051 TGGCAAATTTC TTGTTTTTG TTTTCAGAAG ATAAACCTTA ATTATTGAAA
36101 GGTGGTTTTG TTGGGGATGT GATTCTAGAC TGACAGTTAT TTTCTCTCAG
36151 AACTTTGAAG ATGTCATTCC CCTTCTTTGT CTTCCATTGT TGCTGTCGAG
36201 GAGTTTGCTT TTAGCCTTAT TATCTTCCTT TTGCAAGGTGA TCTCATTTTC
36251 TCTGGATGTT TAAAGACTT TTTTCTTGC CTTTATGATT ATGCAGTTTT
36301 CTCTAGGAGT TGTCCAGTGT GGATTTCTTT TTACTTACCC TGTTTGGTAT
36351 ATCTTGTGTT TCTTCATTG GTGAATTCAT GTCTTCATC AGCCATTTC
36401 TTTTGAAATA TTGACTCTAT TCTATTCTCT CTCTGTAGAG CTCCAATGAA
36451 AGACTATTAG ACCACATTCT TCTGTTATCC ATTTCTTC TCTCCTTCAT
36501 ATTTTCATT TCCTTAACCTT TCTGTGATGC ATTCTGGTA ATTTCTTCAG
36551 CTCATCTACC AGTTCTTAA GTCTCTTTA AACTATGTAT TAGGTTGGTG
36601 CAAAAGTAAT TGCACTTTT GCCATTTAAA GTAATGGCAA AACCATAGTT
36651 GCTTTGCAAT CAACCTATAT CTCTTACCTT TTTACCACAT ATACAAAAAT
36701 GTATGTTATT CTATGAATAA GTGTTTCACTG AATTTAACCA TGAGCAACAA
36751 TGACACAATA TAAAAATGCA GTTATAAGTC AAAATTATTG TTATTACTCT
36801 TATTCAATTCC ATTTGATTGT TGTTTCTG GTAAAACAA AAATGTAATG
36851 TAGAAATAGA ACAATATGCA TCTTCCATTG AGCTCACTAT ATTTGTTTAC
36901 CCTCAAAGTA ATTGCTAGAC CTTGGTATT TACACTGAGA TCCCTCTCCT
36951 CCCATTTTT TCTTTTTCTT TTCAAGGTGA TAAGAGGGGA AGTGAGAAGG
37001 GAGAAGATTG CCAGTTGACA AAGAATGAAA AAGAAAGAAAT AATCCTATT
37051 TGCTAGGCCA TGCAACCCCCA TAGGGTCCAA AGTGAATGCC CTTGTTAGGAG
37101 GTAGATGACA CTGGGTGAGC ATTAGTCAT TTGCTTAAA GAAACCAATT
37151 ATAACCCGTA GTGCAGAGCC TCTCCTTCAC AATGAGGCCT GGTGGCAGCA
37201 GTGTCAGTAG GGGGCCAGAG CAAATAACA GGGGCTCTAG TTAATTATGG
37251 AAAACTTGCA ACTAGGACAT ATTGGTTATT CCCAAAGCTC CCAACCAACA
37301 TTCTCTCATC TTCTGACGTC TTTTCTTCTC TCTCTTCTG CTACCTTTTC
37351 AGACCTTAAA AGATTCATT AGTGACTIONT GTGAGAAAAA TGCAATATT
37401 TAGGATTATT AAATGGTGTG 37451 TACATAAAAT TTACCAATTCA
37451 TACATAAAAT TTACCAATTCA TCACGTTTT CAGGTGTACA ATTCACTGGC
37501 ATTCACTACA TTCACATTGT TGTGTAACCG TCACCACTGT CCATCTCCAG
37551 AACTTTCAT CATCCAAAC TCAAACCTG CACGTATTAA ATGATAATT
37601 CCCATTACCC CCTCTCCTCA GTCCCTGGTA ACCACGATT TGCTTTTTAT
37651 CTTGATGAAT TTGACTATT TTGGTACCTC ATATAAAAGT GGAATCCTAC
37701 AATACCTCTT CTGTGTCTAG CTTGTTTGC TTGGCATAAC ATTTCAAGG
37751 TTCATCCATG TCGTAGTACA CTGAGTTTC CAGAAGCATT TATTCAGTA
37801 CACAAGGTCA TCTATTCACT ATCAGTTCA GGCAGCTGCT GGTGTTAGGA
37851 CTAGAGAAAG TTGTCCTCTGC CTAACAGATC ATTTACTGTC ACATTTCTCG
37901 CTGCAAACCTT CCAAATATAA AAAGGGTGGT CTAGAGAAAA GCAAGTGAGA
37951 ATGTCATGTC ACTGCCATAT ATTACGTTAT TCTGAATTAA CTTCAACAGT
38001 AAGAAATGAA ATACTGATTTC ATTTCTCCC ACAACATTG GATATTCTCC
38051 TTGCACCTCC AAAAAGCCTA AAAACTCCGA GATGGATTGTT TTTCTCCAG
38101 GGACTGCCTA AGGAATCTGA GGAATCTTC CCCCTTTAT GGAAGAATT
38151 GTTCATGCTC AGAATAGAGA AAAAGTAGGA GGAGAACAG AAAGAGGAGA
38201 AAACATCTAA GCAGTTTCCT CTAACCTGAC TGAAGAACCA CATTGGAAC
38251 AATAAAATGA CCCAGCACAT CTCTCCCTC TGGAAGGGTT TAATGTTTGA
38301 TGTACAGGG TCTTTCTCC CCTGCATATG AATTTCCCT TCGTCTACAC
38351 GGGCTGCCCT ACGGGTATCT CCACACAGCA GAAATCCTA GAGAAGCTTA
38401 AAGATATGTA GGGTAAGAGG AGCCCCAGGA ATGAAGATT AAGGACAAAA
38451 CAGAAAAATA AAAGGAAATA GAAGCTGGT CCCTATCTGG ACTTGAATGT

FIGURE 3N

38501 TCAGAATATT TAAAATGTTT GCTTTAAGAA TAGTCTGTGG TGGGCAAAAT
38551 AGATGATAGC CACATGACTT GTATTCCCAA GGGTAAGAAC CAAATTAAAAA
38601 AAAAGAACAA GTTCTGAACA GAAATGAAAA ATAAGATAA ATTGCATAGT
38651 TCTTTTTTTT TATTAGATGG AGTCTGGCTC TGTCGCCAG GCTGGAGTGC
38701 AGTGGTGCGA TGTCGGCTCA CTGCAACCTC CAACTCCCCG GTTCAAGTGA
38751 TTCTCCTGCC TCAACCTCCT GAGTAGCTGG GATTACAGGA ACACACCACC
38801 ATACCCGGCT AATTTTTGGA TTTTTGGTAG AGACGGGGTT TCACCATGTT
38851 GCCCAGGCTG GTCTCGAACT GACCTCATGA TCTGCCGCC TCGGCCTCCC
38901 AAAGTGTAG GATTACAATG CTTACACCTA GAACAGATCT GTCACCTTTC
38951 AAACTTACAG TGTGGGCTTG TTTTGTATC ATGCATTGA TATTACAGT
39001 ACCTATGGAT AGTCATGTA CTGAAATAAA ATTGATTAG GAATTTGTC
39051 TTATAAGTGT TCTAAAGACT TGACAAAGTG CACACATACA CACACTATAT
39101 ACATAGTGTG TGTGCATGTG CGTGTATATA AATGAGTAAC CTTAGACTTA
39151 GATTGTAG ATGAGGAAGG TTTCAACCTT CCCCCAAATG CAAATGGAGA
39201 ATTTCAACCA TATAAACCAA ATATTGGCAT TTTATCTCTG GAACACAAAC
39251 ATCTTGTT ACTTTATGGT ACTTACGTA TGCCCTGAAT GCTCTAGTTT
39301 TTGCCAATAT ATTTTACATA ATTTTGTATA CAAGTTAGT GGTATAGAAG
39351 ATAAAGGACA CTAAGCAGGA TTAACAGCTT GGTTCCCTAC AGCTGTTAAG
39401 TATGAAAACA CACCATGAAA AGGCAACAAG CTTCTTCCAG GCAATGGAAG
39451 GCTTTTGGG GGAGAAAAGA AAGTGAATTA CAGGTTAAA CCTAGGAATG
39501 TCATTTTTG AAACCTGTTT AAAATTTT CAATCCTTCT AGTGGTTTGT
39551 GAGCTCCTGG GGTTTCTGGA AGGTGTTGG GAACCTGGATA GAGGGTTAGT
39601 TCATGCCTT AAAAGCCAAT ACATTTCCAT TTCTCTTTA TAACCAAGTA
39651 ATAACCCAAT TATGCATGTA TTTTATATAC ACAGACACGT ATTATTTTT
39701 ACTCCAAAAC AAAATGGTCT GAGGCCCTTC AAGAAAGTGC ATGTGGCGAA
39751 GTCATGGGGG GCAGGGTGG AACCATTG TGTTGCCAC TAACTAGGTT
39801 TCTCAGTTGG CTTATCTCTT AGTGGACCAT TGCTAGCAAC CAGGGTGT
39851 TTAAGCATTG GACAGTTTC CATCACTTTT ATTTGCCTTC ATATATTGTT
39901 TCATTTACAC CCTTAGTATC TCTTGTTTA AAGACAGGAG ACAAAAAGAA
39951 CATGGATATT TAAATACAAG TTAATGAGGA ACTTTAAAAT AATAATAATT
40001 CTACAAATTT ACCTCAAGAT ACTTTACCA ATTCTATAAGT TACATTTATC
40051 TGATCAAAAT TCTTGTCAT CATATCAAGA TGTTTCTTAT ACAGCAGAAA
40101 TCAGTAGAAA AGAAAAAATA GGCAAGCGT GTGGTGGCTC ACACCTGTAA
40151 TCCCAGTACT TTGGGAGGCC AAGGCAGGAG GATTGCTTGA GGTGGAGT
40201 TCAAGACCAAG CCTGGGCAAC ACAGTGAGAT CCCATCTCTA TTAaaaaAAAT
40251 TAGAAAAGAA AAAGAATAAA ATGGGGCTGT TATATCCAA TTGGCTTTT
40301 AAAAATCAGC AATAAGGCCG GGTGTGGTGG CTCACACCTG TAATTCCAGC
40351 ACTTTGGAAG GCTGAGGCAG GCGGATCAAT TGAGGCCAG AGTTTGAGAC
40401 CAGCCTGGCG AACATGGTGA AACCTGTCT GTACTAAAAA TACAAAAAATT
40451 AGCCAGGCAT GCTGGTGCAT GCCTGTAATC CCAGTTACTC AGGAGGCTGA
40501 GGCAAGGAGAA TCACTTGAAC CTGGGAGGTG GAGGTTCAG TGAGCTGAGA
40551 TTGCACCACT GCACTCCAGC CTGAGTGACA GAGTGAGACC CTGTCTCAA
40601 AAAAAGAAA AAAAATTG GCAATAAAA CAACCTGTTG CTTGCTGGAG
40651 GAAAACCTG CTTGCAAAGC TCAGTCTGAT ATCATTTTT AAACAAAAC
40701 CTAAGAACAA GCCAGTCAGT TAAGCTAAA CAAATTTT GATTATGAAA
40751 AGGGTTTTG TATATTTTA CAGGATAAGA TACAAATAAA TTTCAGTCTT
40801 TCTTTTAATA TGATTTCTG TTCCCAAACC AGACACAAAG CAATTTTAA
40851 ACTTGATCGT CAAGAAATCT GTTTCTCCT ACACAAATCAA TGAAAAGTAA
40901 TCTAAACAGT GTTTGTCAGG CCAGGCACAG TGGCTCACAT CTGTAGTCCT
40951 AGCATTTGG GAGGCCCTAGG CAGGTAGATT GCTTGAGGCC AGAATTTCAA
41001 GACCAGCCTG GACAACATGG CGAAACCCCA TCTGTATTAA AAAAAGAAAAA
41051 AAAAAGAAC CATATGTCTG CAGTCAGATG GAAAAAGTAA AAATATGTAA
41101 TAAACACATA TGAATAATAT TAAGGACCAT ATTAAATTA AACTTGATA
41151 ATAAATTTT AATAATATTA TCTACGATAA AATGTTTAC TAAATTTCG
41201 TTCTTATCA TGCCACACAA AAATGGCAA ATGATTAAGA GAGTTGCAA

FIGURE 30

41251 AATTATGTGG TATAGTGAAA GAGGTTGCG GTTAAAAAAA AAAAAGAGAG
41301 AGAGAGAGAG AAGTATGGGG CCATGGGGAT AGTCTCTGTA ATCAGTCACC
41351 TGAACCACTT TTAATACTCA AAAGACTTAT GAGAATAAAA ATCTGATTTT
41401 TGCTAAGATT TATTAGCAA AATAAATCTTA CTCCTTCCTG TCCCTCTCTA
41451 ATTATCCTTC AGCTTGACCA TGATGAAAG AAAATTTACA TTTCACTGTT
41501 TAATCTATTT AAAGATGAAC ATTTCCCATT AAATCAGGAT GCACCTTATA
41551 ATCAGTAGCA TCTAACAAATA TAAGTCAGCC AGGCTGCAGT TGTGACTGTA
41601 GTTACAATTG CACATGTGTG AACATCAAAT GAGCCAGCAT CAAAACGTGC
41651 AGAATGGCCA GGCACAGTGG CTCACACCTG TGATCCCAGC ACTTTGGGAA
41701 GCTGAGGTGG GTGGATCACT TGAGGTCAAGG ATTCAAGAC CAGCCTGGCC
41751 AAGATGGTGA AATCACGTT CTACTAAAAA TACAAAAAATT AGCCAGGCAT
41801 GGTGGCAGGT GCCTGTAATC CCAGCTACTT GGTAGGCTAA GTCAAGGAGAA
41851 TCGCTTGAAC CTGGGAGGCG GAGGTTGCAG TGAGCTGAGA TCGCACCAC
41901 GCACTCCAGC CTGGCGACA GACCAAGATT CCACAAAAAA AAAAAAAA
41951 ATTGCAGAAT TGGTGTCAAG GACTTGGAAAG AAAATTCTGC AAAGAAAAGT
42001 CCTTTTTTTT TCTTTTTTTT TTAAACTCC TAGGAACCAA ATGGTTGTGG
42051 AGAAGGAGTA AATCAGACAT GTT TAGCAAC ATTCTTTAAG CAGGAGTCAA
42101 AAGTAAGCTA ACACATACATA ACTGCAAGGC CAGCTTAGGA GCCCAGGACC
42151 AATGACTCTC TGTTGTTTTA TGGATTATTT TAAGAAATGC TGCATCATCA
42201 AATTCTTAAT ATAGAGGATG ATACATGGGT AAGTGTAGAC ATCAAAGAGT
42251 CTGAGTCAAA TGCTGAATGT GAAAAAGTTT TAGGAATACC GAAACCAATT
42301 TATTTTGCTT AATGTTCTC TTTTCGTGT ACAAGTATGC TATATGAGAA
42351 AATAATCTCT ATTTAATTAA ATTTATAACA GCCCTTTCAA TAAGTATAAA
42401 ATGAACATTC TGATCATGTC ATAGTTAAC TTGCA TTTTTT TTGTCTTAAT
42451 GGCAAAAAAAC CAATGACGCT TCTTACAATG ATAGCATCTT AGACTCAATG
42501 AAAAGTGGGG ATGAAATGAA ATTTGGGGAT ACAGTACTTT CCCCTCTTCT
42551 CCTAAAACAG ATAATGAGCT TGAATGATCT ACAATGTTTG CTAACTCTAC
42601 TGCTTCTTA ACTGCTGCTC GTGGTGTTC ATTTTAATAA AAAGCTGTGG
42651 GCTGTTCTTA TTTTGTITGA CATAGGGACT TTTTTTTGG CCCAAGACTT
42701 TTAATATCAT GTGGTCCGTA TTTAACTCTC CCTAAAATAT TTCTTGGGAA
42751 GAGAAATTCT AGTAGTTCAAG TTCGCTTGT ATGATTTCTT TCAAAGTGTG
42801 AATTTACTCT TATTTCTTT GCTAGGGGTG CAGGCTGCAT CTTTATTGAA
42851 ATGTTCCAGG GTCAACCTTT GTT CTCGGG GTTTCCAACA TCCTTGAACA
42901 GCTGGAGAAA ATCTGGGAGG TAGGAGAATA ATTCTTCTAA AGAAAATGAA
42951 ATATCTGCAT TTTAAGTTTT GAACCAAATT TGCCCTACAG ACAAATGAAG
43001 CAGTCCATCT GCTCTGAGAT ATTAAGCCCT ATATAAAGAT TGTAGAAACT
43051 GTAGCATTG CCACAGCTAT AAGCACCTG GGAATGTGTG GTCAAGGAAAC
43101 TCCCTGTTGC CCCATAGCAG CCCATGAATC CAGCTCACTG AATGATGTT
43151 AGGTCTCCTG CTCCCTGTCA TTAGTATTGT CTTAACCTCC CAGGGCAATT
43201 TCTGCCATT A CTACTCAGAC ATGTCCTAC CTTGCTACCT CCAGTTCTAA
43251 TGCTACCATA TATTTGGCCC TGGATCTTGT TCAACTGAAA ATAAGACATA
43301 GAAATTTTAG CTGGGTGCAG TGGCTCATGC CTGTAATCCC AGCACTTTGG
43351 GATTGCTTTG AGCCCAAGGAG TTCGAGACCA GCCTGGCAA CATGGCGAAA
43401 CCCCATCCCT ACAAAAACAA AAATGAGTGG GCTGTGTGGC GCACACCTTA
43451 GTCCCAGCTA TTCAGGAGGC TGAGATGGGA GGATCACTTG AGCCCAGGGA
43501 AGTCGAGGCT GCTGTTAGCT GTGACCACGC CACTGCACTC CAGGCTGGGG
43551 AACAAAAAAA AGACACAAAA TTTTCATAGA ACCCTGATAG AACAGAGGCT
43601 TTCCCTCTTA GTGTGAAAGA AGTGTACCAT TTATCATGCT TATCCACAGC
43651 CAAATTCCCTA AAGTGTCAAG GTGCCTTGT GTGTGTATGC AGCTCCATT
43701 CTTAATTCTA TATTTATCCC TACCGCAGTT GCCTATGATA TGCTTTGTTT
43751 TTATGGCCCT TATATAGTAT TACAGTCATA CTATAGTCAT CTGTATATT
43801 CCTTTTTTGG TCATATTTT ATTGTGGTAA AATATACAAA ACAAAATT
43851 CCGTCTTAAC CCTCCTTAAG TGTACAGCTT GTCAGCATT AATACATTCA
43901 TATAGTTGCA CCACCATCAC CGCCATCCAT TTCCAGAACT TCTCTATCAT
43951 CCCTAAGGGA AGCTCTGGAC CCACTGAACA ATAACGTCCCC ATCTTCCCTC

44001 CCCACACTCC CCTAGCCCCT AGTAACCTCT AATCTACTTT CTGTCTCCAT
44051 GAATTGGCCT ATTCTAGGTA CCTCATATAA GTGGAATCAT ACAAAATTTGT
44101 CTTTCCGTAT CTGGCTTATG TCACTTAGCA TATTTTCAGG GTTCATCCAT
44151 GTTGTAGAAT GTGTCAGGG GCTTTAAATC GGCGGGGTGC AGGGGGGTAC
44201 TTTTATTACTT GCTATCCTGG ATCCTGCTGC TTGCTTCTG GCTAAAATAA
44251 AATGTACTTT GTGAAATTAA GACATTTAT AGAGATTAAT TACTGACATT
44301 AAATTTTCTT CTAGAACAT GGGGGCTATT ATGAAGGAAC ATGGGAAAAAA
44351 CTGGGAAGCA TTCACAAC TG AAAAAAAA ATCCAAGCCA AAAGACTTTT
44401 TCTAAAAACT TTCTTGCAAG ACAGAGCAAT GCTATCTTC CATTATGTTA
44451 TTGGGTGCTA TAACATCATC TAAGCTGGAG ACAGCCTACT GTCATAGCTT
44501 TGAGGTCCAA AGACCTGGGT TTGAATTCTA ACCATTTCT AGCTAAATGA
44551 ACATGGGCAA GTTATGTAGT CCCTCTGAAC TTTCGTTTCC TTGTCTGTAA
44601 AATGGCAACA ATGATAATAA GGACTTTCTA ATTCTTTATT GAGAATTCCA
44651 TAAAAACAAA TGCATAACAA GCTCCATGCA CCATAAATGC TCAATAGATG
44701 CTTGCTTCTC TCCTGTCCCA TACAAATTGT TGTACAGATG TTTCAATAAC
44751 CTAAC TGCTA GCAAGTATTA CCTGAAATT AACCCGATTG TTCTCTTCTT
44801 TCACTTAGCA GTATTATTC TTGTCACAA TAGAGGAAGC ACAATTGCAG
44851 TTCTGATGCT GCAATGACCT TTTATACATT TGAAGAGTTT TTCTGGTCA
44901 TTTAATCAGG AAACAACACT TACTCACCAT ATATGAGGCG AGTAACCTCA
44951 CAAGACTCTA CAAGGTCTTG TAAGAAGCTA TAAGCCAAGG GGGAAAAAAA
45001 AAAGAAGAAT AAGAAAAACA CATGATCTGT ATTTCAAGT GTTGTTCAGT
45051 CTAGGTAGGG CGATGGGTGA AGTATACGTA AATATATGTG AAACAAACAT
45101 AAACTATGTA TATATGTAAA AGGATGTATG TATAGATAGT TAATATAAAAT
45151 TGTAACTTG AAATAAGATG TGCTATTAGG ATACTTGAG AGTAGTTTAT
45201 TTGAAAAGAA TATAAGTATA TCCCTGTGTG CCATTAGTAT TTGAAGAGTT
45251 GTATATAAAC TGATTTTTT TCTTTTCTT TTTTTTGAG AAGGAGTCTT
45301 GCTCTGTCA CCAGGCTGGA GTGCAGTGGT GCCATCTCGG CTCACTGCAA
45351 GCTCCACCTC CCCAGTTCAA GCGATTCTCC TGCCCTCAGCC TCCTGACTAG
45401 CTGGAATTAC AGGTGCCCGC CACCACACCT GGCTAACCTT TGTTTTTA
45451 GTAGAGACGG GGTTTCACCA TGTTGGTCAG GCTGGCTCA AACTCCTGAC
45501 CTCGTGATCC ACCCGCTTG GCCTCCAAA GTGGTGGGAT TACAGGCGTG
45551 AGCCACCGCG CCCAGCCTCA TAAACTGATT TTTAAAATAC AATATACAGT
45601 TAGGCATAGT TGTGTGTGCC TATAGTCCCT ACTGCTTGGG AGGCTGAGGC
45651 AGGAGGATCC TTTGATCCCA GGAGTTGGG CAACATAGTG AGACCCCCAT
45701 CTCTAATAAT AATAAAATATA AATTTCAAAT AACATTTAA AATATGACAT
45751 ACTATCTTG AATGACCACA CAATTTAAA AGCAATCATT TTACGGTTCT
45801 TTAGTGTTC A GTTACACAG CACTTAGAA TCATAGAATA AAGTGAGCAA
45851 GATGCTTCTC AAAGCCTGAT CACTCTTCTG GACTCACAAT GGGCTAGGTA
45901 CTATGCTGGA AAGAGAAAA ATAATAATT TCTAACCTGC TTGAGACATA
45951 GTGGTATAAA TGATAACACA GCTGCTGAAC GTGATGACTT TCTCACTTTG
46001 TCCGCAGAGC AAGAAACTAT AGATGCAGTA ACAAAACTGC ATTCAATGAA
46051 CATGGGACTG TAGATAACAA ACTAACTTCA TTTCTTGGG TACATGCCCT
46101 GTATTGGAT TGCTGGATCA TATGGTAGTT CCATTTTAA TTTTTGAGG
46151 AACCTCCATA CCATCTTCCA TAATGGCTGT GCTATTTGCA TGCCCAACAT
46201 CAGTGTGCAA ATGCTCCCTT TCCTCCACAT TCTTGCAAC ACCTCTTCA
46251 TCTTTTGAT AATAGTTATG AGGCAATATC TCACCATGGT CCTAGACTTC
46301 ATTTGTCTGA TGACTAATGA TATTGAGCAT TTTTTCATAT ATCTCTTGGC
46351 CATTGTAGG TCATCTTTG AGAAATGTGT ATTGAGGTT TTAGTCCATT
46401 CCTGCTACCA TAACAAAATC CCTTAGAGTG GGCATTTAT AAAGAACAGA
46451 ATTGGCCCGG GGCAGTGG CTCATGCCTG TAATCCCAGC ACTTTGGGAG
46501 GCCAAGGTGG GTGGATCACC TGAGGTCAAG GAGTCAGC CAGCCTGGTC
46551 AATATGGTGA AACCCCATCT CTACTAAAAA TACAAAAACT AGCCGAACGT
46601 GGTGGTGTGC ACCTGTAGTC CCAGCTACTT GGGAGGCTGA GACAGGAGAA
46651 TTGCTTGAAC CCAGGAGGAG GAGGTTGCAG TGAGACGAGA TCGTGCCACT
46701 GCACTCCAGC CTGAGCAACA GAGTGAGACT TCATCTCAA AAAAAAAA

FIGURE 3Q

46751 AAAAAAAA AAAGAACAGA AATTTATTC TCACTGTTCT AGAGGGCTGGA
46801 AAGTCCAAGA TCAAGGCACT GTAGGCTGTT GTCCAGTGAG TATATTTGGT
46851 CTCCAAGTTA GTGCCTTGTG C GCTGCATCCT CCAGATAGGG CAAATGCTGT
46901 GTCCCTTACAT GGTGGAAGGG TAGAAGAGCA AACGGGCCTG ACTGATTCCC
46951 TCTAGCTCCT TTATAAGGGC ATTCATCTCT GTCCCTGTGT CCTAATCACA
47001 CGCTAAAGGT GGCTAAAGGC CCCACCTCTT AATACTGTT CATTGGGGAT
47051 AAAGTTTCAA CATGAATTAT GAAGAGAATA CAAACATTAA ACCACAAACA
47101 AGTCCTTTCGC CCACTTTTT TTTGGAGACC GAGTCTCACT CTGTTGCCA
47151 GGCTGGAATG CAGTGGCTTG ATCCTGGCTC ATTGCAACCT CCACCTCCTG
47201 GGTTCAAGCA ATTCTCCTGC CTCAGCTTCC CAAGTAGCTG GGATTACAGG
47251 TGTGCACTAC CACACCCAGC TAATTTGTA TATTTAGTAG AGACAGGGTT
47301 TTACCATGTT AGCCAGGCTG ATCTCGAATCT CTCGACTTCT GGTGATCCAC
47351 CTGCCTCAGC CTCCCAAAGT GCTGAGATT CAGGCGTGAG CCACCGTGCC
47401 CGGCCCTTTG CCCACTGTT AATGGGGTTG TCTTCTTGCT ATTGAGTTCC
47451 TTATATATT TTTATATTAA CCCCTTATCA AATGTATGGC TTGCAAATAT
47501 TTTCTCCCAT CGTAGGTTGT CTCTTCACTC TAATGATTGT TTCCCTTGCT
47551 CTGAAGACAC TTTTTAGTT TATTTATTCC CATTGTCTA TTTTCACATT
47601 TGTGCTTAT AAGCAGGTTA GAAAATTATA CAGATTATAA ATAGTTCTG
47651 AATTTGTGTT TTACTAAACG TAGCCTACAC AGATGAAAAG AGGAAAGCTA
47701 CACTTCAGAA TCTGTGATAT TTGATGTCAG AAGTGCATCC CTGAAAGCAA
47751 TGGGTCCATT CTAATCTCC TAACCTCTAA CCATAATTG TTCTATATTT
47801 ATCCTGAGAT CTCACTCTTA GGAATAAAAA CACATTGAGA AGTCCTGAGT
47851 CTCTATTTTA CTATTTTCT GAAGTGCCTG TAGTGTGTT GTTACATCT
47901 AAATAATAGC TGTCAACACT TTCTGATCAA TTTAAAAAC TAATTTAAA
47951 TAAGTGTTT TCATAAATAA TCCCTGGATT AGTTCTAAA TCAGAATAAA
48001 CTATGAAAC TTTGAATCCA TTAATCAAA TGCTTTAGT TTCCATTCCA
48051 ACAAAAGGCGAG ATAAACAGCC CCTTCAGACC ACTGTGGTTT GAAACATAGC
48101 ACTCACTGGC TGCCTTTAA GAGCCTTCAG GGAGGGAGCA AAACAACAAT
48151 TTTTGGTTTT CAGTTTCCCA GACAGTGAAG GAGAGATTAA GTAATTTCT
48201 CAAGTAAAAA AGAATTCAAT AACTTGAAA TAGAAACTGA GATCAAATT
48251 CCAAATAAAAG TATATTGAAT TTTTGTAA ACTTTAAA TCTCAAGCTT
48301 AAAGCTTGA ACATAAGATT AAAAAGACTT TTTTGTAT CCATTTGTT
48351 GGCTTGTGTT AAATATCATA CAAAGTAACC AACCATCTGG TAACTTTCAC
48401 CTTAGAGAAA ACATGATAGT GGTTGTCACC TATTTCTTCT ATTGTTTCT
48451 CTTCATTATC TTTGCTTTCT TTTCAGTCA CTTTGCAGC CAACAGAGGA
48501 TGTATGGGTA CATGTGACTC ACACCCACTT GTTACACAT GCATCTGTGC
48551 AAATACATAA GATGGTAGGT TAAAAAAAGA AGAATTAGTT TCTTGTCCCC
48601 TGGCCTTCTC CCACAAAAGA AGAATTAGTC CAGTTGGTTT TTCAAAATGG
48651 ATTCAGGAT TCTTAGTGTG CCTCTGGGCT CAGGGTGGTT GATAGGAAAA
48701 GCCTATAATC CTCTCAGTCA CTTTTCAGTT TGTGGTAGGA ATGGATCAA
48751 GAAGGAAGAT TTTACTGGGT GGCATGATT TTTTATTATA TGAGGGAAAA
48801 TAGCACTTCA CTGCTTTTG TTTAAAGACA AGCTTAACAG ATGCTAAAAA
48851 GTACATCTCT CAGCCAGATT CCTAGTCAAC AAGCTGATAG ACACTAAGAT
48901 TCTGGATTCT TCATTGATTA TATTCACTCA TTGTTGGCA ATTGACTCCC
48951 TGCCATAATA ATTGGGCCAG TATCTATAAC CAGCATTAA CAGATGGATT
49001 CGCTAGACTC TTTCTGTAAG AGATGTTCT AAAAAGAGTT ATAGTGAGAT
49051 ATGCTTCTAA GAAAAGTTAT ACTGTAGTAG TGTAATGAAA GCTACTAGTG
49101 TTTTATTAGT ATTTCACAAG AACAAATGTTA CTCTGTCTCC CATATATAAC
49151 TGTCTATGGG CTTTTATGAT TATTCTTAA AAAAAAAA TACTAAGGTA
49201 ATGCCTACCG GGGAACTCAT GGTGCTGGCT TCATCCAAAG TCTGAGCTGT
49251 TTTGGCTTTA TACTCCGAAA GACTTTATT TCATACATCT TAACTAAAAA
49301 CTGGGGCTTT AAATTGGTCA TTCAAGGCCA GGCGCGGTTG CTCATGCCCTG
49351 AAATCCCAGC ACTTTGGGAG GCCGAGGTGG GCAGATCACG AGGTCAGGAG
49401 ATTGAGACCA TCCTGGCCAA CACGGTGAAA CCCCGTCTCT ACTAAAAATA
49451 CAACAACAAAC AACAAACAAA ATAGCCAGGC GTGGTGGCTT GCATCTGTAA

FIGURE 3R

49501 TCCCAGCTAC TCAGGGAGGCT GAGGCAGGAG AATGGTGTGA ACCTGGGAGG
49551 CAGAGCTTGC AGTGAGCCGA GATCGCATCA CTGCACTCCA GCCTGGGCGA
49601 CAGAGCGAGA CTCCGTCCTCA AAAAAAAA ACATCGGTAA TTCAAAGCAT
49651 AGACCAGCCC TTTTCAAGT GATGTTGTTG CCATGACAAT CCATCAGTGA
49701 AAAACCAAAT ACCATATTCC AAGCTGCTAG TCACAGAGAA ACAAGCAGA
49751 TGAGATGAAT GTAATAGAAA AGACTAGAGT TAGTTTGGG GTCACTTTA
49801 GCCAACATTC CATTGCTGTA AGCTCAGTAA TCTGAATCCT TTTAATTG
49851 AGCACATCAG GGAACAGCTG AATACCCATG CTGAGGCATA ATTAAGCTG
49901 TCAAGTGTCT CCTGTCATAA TACATGTGGT CATCTGATGC AAGGCAAAGA
49951 GACAGTCACT CCTGCTTCTT TATATCCCTA GCTCCAAACA TGGTGTCTA
50001 ATGCATGATA ATCATGCAGT AAATGTTCAAG TGATGAGAAC ATGACTTTGA
50051 GCAAGGCTGT ATGATCTGCC TCAGAACAAAG TGAGTCAGTA AGAATGCAGG
50101 CCCCGGACCA TAGGAATGTA TTACAGTTT GCCCAAGAAA CCACAAACGT
50151 TGAAACACT CAAGTTCTT TCTCGTATAC ATCAGCTGGT GTCATGCAAT
50201 GGGACATACC ATCTGACGCT TCCCTGTTCT TCCCTGATTT GTCCTGCATG
50251 TCTCCAATAC CTCTTCCAA CCACCTCATC TCCCCACCTC ACCTTTCTT
50301 TTCTTGTTT GGCTTATAT AGGTGCTGGG AGTCCCTACA GAGGATACTT
50351 GCCCGGGAGT CTCCAAGCTA CCTAACTACA ATCCAGGTA TATTGATCTG
50401 AGCTTCTGAA TACTCTGAGA ATTAGTAATG TAAGGAGAGC ATTGGCCACG
50451 CTAACAGGGC GTTCTTGTAT TGTGAECTA GCGGCAAAGA TGGGTGTAGA
50501 GGAATTCTA CATTCAATAA TTCCCTGACT AATCTTTGTA TGAGGAAGAC
50551 ACTGAAAGAG TAGCTGAGGT TAGACCAGTT CCCAGCTCT GTAAAACACA
50601 AGTAGCAAGC TGAATAGAAAT TTGAAATGAC TATTACTGTG GATTCCACAT
50651 CCATTGTCAA ATACCCAATG GCTAAAAGA ACAACTCAA AGATGGGCTC
50701 ACTTTTGGGC CCCCTGACTG TCATAAGTGT ATTGATTAGT ATTGAATTGC
50751 ATATGTATAA AAAGAAAGCT AATGCAACAG AACAGAGGTA GAGGCTCGCT
50801 AGGCCTAGGA CATGCCAAGT AAGCTGCTG TAGGTTATAC TTACTAAGAG
50851 TTCATTCAATT GCCTGTAAAC CTGACACTG GTCATTGTCT CTCACACATT
50901 TCATCTTCA AGACTGGCTT CTGGGATCGA TTTAGAAGTG CTGGAAGTGT
50951 TATCCATGGG GGAATTCTT GAGAAGCTGT CGCAGGGCCA CATCAGAGGG
51001 ATCAGATTAA GCAGTAGTCA CTTCAAGGAT GTTGAGACAG AGGGGAGGAG
51051 ACAGGCACTG AACTACAGGA TGAAGGATCA TATTAGAAGC TGAAGAAGCA
51101 AATAAAGCCC ATGCCAAAGC TGAGCTCTCA CTGGCAGGGT TGAAGGGGAG
51151 GTAGAAAGGT ACAGATAACG ACAAGATTAG GGTGGATATG CTCCAAGCCA
51201 GATTTTCTA GTCTTATGG TCTTACATTG TTCCATTACT AAAAATGAAA
51251 TCTTCCCAA TTGTTGTCTT TACTTTTTT TTTTTTTTG TGAGATGGAG
51301 TTTGCTCTT ATCGCCCAAGG CTGGAGTGCA GTGGCACGAT CTCGGCTCAC
51351 TGCACCTCC ACCTCTGGG TTCAAGCAAT TCTCCTGCC CAGCCTCCCC
51401 AAGTAGCTGG GACTACAGGC ACCCGCCACC ATGCCAGCT AATTTTTGT
51451 ATTTTAGTA GAGATGAGGT TTCACCATGT TGGCCAGGCT GGTCTCGAAC
51501 TCCTGACCTC AGGTGATCCA CTTGCTTCAG CTTCCAAA TGCTGGGATT
51551 ACAGGCATGA GCCAGCGCGC CTGGCTGTG GTCCTTAFTA ACTTTGGTAT
51601 GAGATTATCC TGGAAGGGTT TCCTGAGAGC AAGAAATTGT AGGTAGAGTT
51651 AAAATGTGAT TAAAGAAGAG AATAAAATAC ATAGGGAGCT GGGGACTCTT
51701 TTTCTTATT TCTTGTGAT CCAATACTTT TGCTTACAGC TATCCATAGG
51751 GATCTGGCAT CTTGAACCAC CAGGATTATG GAAGCCCTAC AGCAAGCTAA
51801 AGACTAAGTC TAAAGTCCTT TCAGCTGCTT TGTGAATGGT TATATCTATT
51851 GCTAAAAGGC CTTAATATCA TTTGCAAATA GTTTATGATT TCTAACTATT
51901 TTTCTAGAGT TTAACACGTG AGAAAATGC TACTCTCTGG TCACAGGACT
51951 TAGAATAGTG CCTATTCCA TTGGTCTGAG ATAGAGAAAA AAGAACAAAGT
52001 TTCTTGTGGA GCCGTTGTCAGT CTGTCAGTAA TTGCTCCTAT CTCCAGTTGC
52051 CATGGTTTCC AGGAGAACGT GGCTCTCATC TTTCTGCCC CTGCTGTAC
52101 TTCTCCCTGT CCACTCTGTT CTCTATTTC CCTCAGCTTC CTAACGTAGG
52151 ATGCCAGCAG AAGTTTAGAG TCACAGATGG ATTGTAGGAA ACAATTGGAA
52201 TGATGCCAAT ACAAAAGCTAC TGTGGTGGC ATATGCTGCT CCCCCAAACT

FIGURE 3S

52251 TCAGACATTG GGGTTTCAGG TTGGTCCAGG CAATCAACAG TGATCCTTAA
52301 TACAAAATGT CTTGGTGAGA GCAATAATCA AGAAACTTGG CCAAAGTGCT
52351 TCCCTGCCAG ATTGTGTGCT TAATAAGATA ACTGGGTTCC AATAAAACAG
52401 AGAAAATATG TTACATTTTA AAAAATTTTC TGTTGTTCA AAACAATGTG
52451 CAGTTTTCT ATATAAGAAG AAAAGTCTCC AGGCCAACA TCCATAGGGC
52501 TCATCATCCA TTGTTTTCT TTTAAGTTT CAATTAATC CAAATAAGTC
52551 AAAAATTTTC AGGTACCTAC TATCTGCCAG GTGCTGTGCC GTGCGCTGGG
52601 GCTACACAGA TGGAGAGGGT GCATTCTGG ATCTCTAGTG TTTGGGTTT
52651 GATTCAATTCA CCCACACTCT TTCACCAGTT CTCTTTGTTA CTGGGGTGCT
52701 CATTGTGAG CCCTGCTTCC ATGGCTTGGA GAGTTTGTTG CTGTGGGCCA
52751 GGCTGAGCTT ATGGAGCAAA GGGAGTTGGA ACCTTAGCCA TAGACATGAT
52801 GTCTAACCTT GGATTGGAA ATCTTAAAG TCCAGCCTAT CTTGGGCCAT
52851 GGGGTCAAGTA TTATTGATAA CTCATCCCAG AGGACTGTGT TTTAAAAGGG
52901 TCTCCAACAT CTGCATTTCA GGAACATCCT CTTACGTGAG TCAATAAGTT
52951 CCTTTTGAGC CACCCCCCTAC CCATCCCCAT CCCTGAGCTG CTGTGGCTTC
53001 TAAACACTTG AATGTCAGTG ATTAAGGGGA GCAGAAGACA AGCTGGGAGC
53051 CAGGAAAGTG TCACAGATGA GCACCGTGT AGCAGCATTG TGGATGAGCT
53101 TCCCATTCTT TTCCCTTTCA TTCTAAGTAG TCCTAGGAGC CCCCCAAACTT
53151 TGAATCAGCC AGTACAATT TGAGGGAGTC CAGTTGTCCG GAACTTGGGA
53201 GAACCATCCA GTGTCCATCT ACACCCATGC CTCCATTCTT AGGCCTTATC
53251 TGACACCTC TAGGAGGACA GCAAAGTTTC CATTGTACA GCTTTAAAAA
53301 AGTCACCTGA TGCTGACCCA GTCGGATTTTC TC (SEQ ID NO:3)

FEATURES:

Start: 2118
Exon: 2118-2240
Intron: 2241-2946
Exon: 2947-3096
Intron: 3097-3310
Exon: 3311-3405
Intron: 3406-7938
Exon: 7939-8018
Intron: 8019-18260
Exon: 18261-18355
Intron: 18356-19116
Exon: 19117-19179
Intron: 19180-29296
Exon: 29297-29420
Intron: 29421-31091
Exon: 31092-31212
Intron: 31213-42825
Exon: 42826-42919
Intron: 42920-50322
Exon: 50323-50406
Stop: 50407

CHROMOSOME MAP POSITION:
Chromosome 2

ALLELIC VARIANTS (SNPs):

FIGURE 3T

DNA

Position	Major	Minor	Domain
864	C	T	Beyond ORF(5')
2111	C	G	Beyond ORF(5')
3259	C	T	Intron
3673	A	G	Intron
3747	A	G	Intron
3788	T	G	Intron
8034	T	A	Intron
27740	G	C	Intron
27752	C	T	Intron
29927	T	C	Intron
30772	A	G	Intron
36310	T	G	Intron
36327	T	C	Intron
40618	T	C	Intron
40928	T	C	Intron
41044	A	-	Intron
41311	-	G A	Intron
41313	-	A G	Intron
44701	C	A	Intron
46020	T	C	Intron
46036	A	G	Intron
46095	T	A	Intron
47608	T	G	Intron
51949	-	C	Beyond ORF(3')
52150	G	A	Beyond ORF(3')
52426	-	T	Beyond ORF(3')

Additional SNPs 3' of the ORF (DNA positions refer to the genomic sequence provided in U.S. Serial No. 60/265,151, Attorney Docket No. CL001098-PROV, filed January 31, 2001):

56707	-	T
57444	A	G
58021	A	G
58064	A	C
59067	T	C G
60034	A	G
63709	A	T
63817	G	A
64845	A	-
64848	G	-
64914	G	T
67367	G	A
67497	T	A
68252	G	-
68580	C	G
69990	G	A
71472	A	G
71664	T	A
71677	A	G
72590	T	C
72757	G	C
72863	A	C
74565	C	T

FIGURE 3U

74850	A	G
75462	G	C
76045	A	G
79973	G	A
83181	-	T
84935	C	T
87476	C	G

Context:

FIGURE 3V

3747 CCCGCCCAATTCATATTATAAAGCCAGGTGAGACATCATAGAACCTAGACTCAGGACCTGTGCAAGACACCAGGCCAGGGAGAGAGACATGATAACTAAACAGCCTTGAAAGAAAAACAAACCTGCCTGCCCTAATTAAAATCAGCCACTTAAATGTTATCAGCCTTCCCTTCTTGCAATTCAATTAGAAGAATTCAAAGAAATAGACATTCTACTACTGACCCAAAGAACATTATCACTCTCAGGCCGTGGGAGGCACAGTTGGTAAAGCGTCTCT[A,G]
 ACAGGTTTTTATATCCCTCCCTAAATCACAATGACAGAGTTGTAATGGCAACCTGGAATTTGCTGCTTCACTCCACCTGGCCTTATAGAAGAAACTGAAGTTGGTTCTGCAAATTATGGTACATGAAAAGATGATAAACTCTAGATTTTATATTGCAAATACACAAAATGTCGGAGAATAAAAATACTGCTTATCCAAAAGCTAAGTACTAATTGGTAAACAAACCAACTTGTAAATATGTAAAAGATCCATGAATTCCCTTTAGTCAAGGTGGGAAAG

3788 CATAGAACGTTCATAGCACTCAGGACCTGTGCAAGACACCATGGCCAGGGAGAGAGACATGATAACTAAACAGCCTGAAAGAAAAACAAACCTGCCTGCCCTAATTAAAATCAGCCTCAATTGTTATCAGCCTTCCCTTCTTGCAATTCAATTAGAAGAATTCAAAGAAAATAGACATTCTACTACTGACCCAAAGAACATTATCACTCTCAGGCCGTGGGAGGCAAGTTGGTAAAGCGTCTCAACAGGTTTATATCCCTCCCTAAATCACATGACAGAG[T,G]
 TTTGTAATGGCAACCTGGAATTGCTGCTTCACTCCACCTGGCCTTATAGAAGAAAATGAAAGTTCTGCAAATTATGGTACATGAAAAGATGATAAACTCTAGATTTTATATTGCAAATACACAAAATGTCGGAGAATAAAAATACTGCTTATCCAAAAGCTAAGTACTAATTGGTAAACAAACCAACTTGTAAATATGTAAAAGATCCATGAATTCCCTTTAGTCAAGGTGGGAAAGTTGGATGGTCGTTTATGTTACTCCAATAGAGAG

8034 CACTTAGTAAAGAGGGAAAATGCTTGGAAATTATATGTATTATGTATTGATACATGTTAAACTTTTATTGAGAAAATTATAGATTATATGCTAGAATTATATTGAAAGTGAAAGTCTTGTAAAGCCATCTTGGTATAAAATTGCTGCTTGAACCACCTCAATAAGTGTGTGCCCTCAATCCTCTCTAGAATAAAATGGACAACTAGTGGCTTAAAAGTCATCAGATGAATGCAGAGGAAGGAGTCCCATACAGCTATCCGAGAAGGTAAAGAACAGCAGAA[T,A]
 TGGACCAATAGATCTGTTTGAGTCCTGATTGGTAAAAATGTATTGCTTGTAAAGTGTAAAGGAGTCTCTCTGGAGAATTACATAATTACATTATTTTATTTTATACAAATTTCAAGAAATTACACTGCTATTATTACTTAATTGGAGAATTGAGATTAAAACTATTATACACTGACCAAAACTATAAATTCACTGAGCAATTACTAATAACTTCCATGTGTTGGCCTATGCTAGGTGCTAAGGCTACCTATATAACCTCAGAAAATTCCATA

27740 CCTGTCTTCTATCCACCTGTCTCCCTTCCCTTCCCTAGTCCTGCATATTGAAAACATTTTTTTTTTGAGATGGAGTCCTGCTCTGCCACCCAGGCTGGAGTCAGAGGCAAGATCCTGGCTCACTGCAACCTCTGCCCTCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCGAGTAGCTGGATTATAAGCATATACCACACATCTGGCTAATTGGTATTGAGTAGAGATGGGATTATAAGCATACCTGGCAGGCTGGCTCGAACCTCTGACCTCAGGTGATC[G,C]
 GCTCGCTTGGCCTTCCAAAGTGCTGGGATTATAGGCCTGGCCACTGCGCCAGTCTGAAAACTGCTTGTCTTGTCTTACCTGGAATTAAAGCTGTTGTTGAGTGGTAAAGCTGTTGTTGATTACCTTCCATGGACATTATTTATAACCAATCAGAAGGTTAAATGTCAGTGAGGATGGCTATGGAAAGCTCCTGGCTGGTGAATGGTAAAGATGAATAATGTGTATATTGAGAAGTGGCTAGGTGCTAAGGCTACCTATATAACCTCAGAAAATTCCATA

27752 CCACCTGTCTCCCTTCCCTTCCCTAGTCCTGCATATTGAAAACATTTTTTTTTTGAGATGGAGTCCTGCTCTGCCACCCAGGCTGGAGTCAGAGGCAAGATCCTGGCTCACTGCAACCTCTGCCCTCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCGAGTAGCTGGATTATAAGCATATACCACACATCTGGCTAATTGGTATTGAGTAGAGATGGAGTTACCTGGCAGGCTGGCTCGAACCTCTGACCTCAGGTGATCGGCTCGCTTGG[C,T]
 CTTCCAAAGTGCTGGGATTATAGGCCTGGCCACTGCGCCAGTCTGAAAACGTATTAAAGCACATACTCGTATCTCTTGCTTTACCTGGAATTAAAGCTGGTTGTTGATTACCTTTCCATGGACATTATTTATAACCAATCAGAAGGTTAAATGTCAGTGAGGAATTGGCTATGGAAAGCTCCTGGCTGGTGAATGGTAAAGATGAATAATGTGTATATTGAGAAGCATCAGAAAGAGAAAATGCTGGGAAGATTGATAGAACCCAGTTAACATTGAAC

29927 TAGTCAGATGGCAAAAGCTGGCACCCCTGCTGCCCACTGCCAGTTGATAGAGA

FIGURE 3W

CATTGGTAGAGTAACTGTACTTAGTAAGTTCTAAATCTAAGTGAATATAACAAATTA
 TATTGGAATAGATTGAGATTATCCCAAGATGATAAAGAGGTTAACCCCAGATTGTAGCAT
 GGACTCCTGTCAAGGATGGAGACTCCAGGACACTTGTCTGCCTCACCTTCTTATA
 TAAGTGTGAGATGCAAAGTTTATTCCATTAAAGTGAAGCAGATTCTCTAAGTATCA
 [T, C]
 TGTATCCTCCATTTAGCACTTATCGCAGTTATAATTATTCACACACATAAATACA
 TACATGCATACATACAAATATATACATGTGTGAGCACACCCCCACACACAAATATATA
 TAGATTTCGCTGATGATTTGTCTCACTGGACTGTAAGCATAATGAGGGCAGCCTGGGT
 TTGTCTTGCTTATCATTTATCCTTAGTGCCTGGTACCATAGTAGGTGCTTAATAAGTA
 CTTGTTGAAAAACTGGCTCTATGTGAGCTAAGGAACCACTCTCTGTGTTGGCAGATGC

30772 CAGTCCCTACGTTTATCTACTAAACTGGCTTCTGGAGTGCACAAACGGAAAGGTGGC
 CATGTTAGTCATGAACAGCTCAGTTCTGTTACAGAGACCCAAAATTACAGAGGTATAAC
 ATGCTAGAAACTTAACCTTCTTCGATCACAGTCTGACCTAACGAGGAGCATGTA
 TGGTGGCCCCATGCTATCTTGGCCAGGCTGCTTCTGTCACGTGGCTCTCCATCCCCAA
 TTGTATGTTCAAGATGGCTGCCACTTCTGCTCATCACAGCCCAGAGGGAGGGAGAAAAG
 [A, G]
 GAAGCAGAACCTTAACCCCTCCAATAGGCATAATCTGGAAGTTCACACATCACCTCTG
 TTCATATCATATAGGCAAGAACTTAGTCACCTGACCACACCCAGCTGCCAGAAGGCCAC
 ATCTAGCTGAAAGCAGGCCAAATTGAGAAATTCACTTGATGAAGTGTAGACAGAG
 TCAAGATAGTGTAGTTCTACTAAAAGCACCTAAAGTTGTGTGTTATTTTCTAATG
 GTGTTACCCGGTCCAGTGCATCATGGTCAAGGCCAGGTTCCAGAACGATGGGTTTAT

36310 TAGAGTGTGTTGTTGTTGTGTGTGAGGCTGCTGGGCAAATTCTCGTTT
 GTTTTCAAGAGATAAACCTAATTATTGAAAGGTGTTTGTGTTGGGATGTGATTCAGA
 CTGACAGTTATTTCTCTCAGAACCTTGAAGATGTCATCCCCCTCTTGTCTTCATTG
 TTGCTGTCAGGGAGTTGCTTTAGCCTTATTATCTTCCCTTGCAGGTGATCTCATTT
 CTCTGGATGTTAAAGACTTTTCTTGCCTTATGATTATGCAGTTCTCTAGGAG
 [T, G]
 TGTCAGTGTGGATTTCTTTTACTTACCCCTGTTGGTATATCTGTGTTCTCCATT
 GTGAAATTCACTGTTCTCAGCCATTTCCTTGAATATTGACTCTATTCTATTCTCT
 CTCTGTAGAGCTCAATGAAAGACTATTAGACCACATTCTCTGTTATCCATTCTCT
 TCTCCTCATATTTCATTTCTAATTTCTGATGCTCAGGTTCAATTCTGGTAATTCTCAG
 CTCATCTACCACTTAAAGTCTCTAAACTATGTATTAGGTTGGTCAAAAGTAAT

36327 TTTGTGTGTGTGAGGCTGCTGGGCAAATTCTCGTTTGTGTTCTCAGAACGATAAAC
 CCTAATTATTGAAAGGTGTTTGTGTTGGGATGTGATTCTAGACTGACAGTTATTCTC
 TCAGAACCTTGAAGATGTCATCCCCCTCTTGTCTCCATTGTTGCTGTCAGGGAGTT
 GCTTTAGCCTTATTATCTTCTTGCAGGTGATCTCATTCTCTGGATGTTAAAG
 ACTTTTCTTGCCTTATGATTATGCAGTTCTCTAGGAGTTGTCCAGTGTGGATT
 [T, C]
 TTTTACTTACCCCTGTTGGTATATCTGTGTTCTCCATTGTGAATTCACTGCTTT
 ATCAGCCATTCTTCTTGAATATTGACTCTATTCTATTCTCTGTAGAGCTCAAT
 GAAAGACTATTAGACCACATTCTCTGTTATCCATTCTCTCTCCATTCTCATATTCTC
 ATTCTCTAATTTCTGATGCTCAGGTTCAATTCTCAGCTCATCTACCACTTCT
 TAAGTCTCTAAACTATGTATTAGGTTGGTCAAAAGTAATTGCAAGTTTGCATTA

40618 CGGGGTGTGGGCTCACACCTGTAATCCAGCATTGGAAAGGCTGAGGCAGGGGATC
 AATTGAGGCCAAGAGTTGAGACCAGCCTGGCAGACATGGTAAACCCCTGCTGTACTAA
 AAATACAAAATTAGCCAGGCATGCTGGTGCATGCCGTAACTCCAGTTACTCAGGAGC
 TGAGGCAGGAGAATCACTGAACTGGAGGTGGAGGTTGAGCTGAGCTGAGATTGCACC
 ACTGCACTCCAGCCTGAGTGCAGAGTGAGACCCCTGCTCAAAAAAGAAAAAAA
 [T, C]
 TGGCAATAAAAACAACCTGTTGCTTGCTGGAGGAAAAACCTGCTTGCAAGCTCAGTC
 ATATCATTTTAAACAAAACCTCAAGAACACAAGCCAGTCAGTTAGCTAAACCAAAATAT
 TTGATTATGAAAAGGGTTTGTATATTTCAGGATAAGATAACAAATAATTCTAGTC
 TTTCTTTAATATGTATTCTGTTCCAAACCAAGACACAAAGCAATTAAACTTGATC
 GTCAAGAAATCTGTTCTCCTACACAATCAATGAAAAGTAATCTAAACAGTGTGTTCA

40928 AAACAACCTGTTGCTGGAGGAAAAACCTGCTGCAAAGCTCAGTCTGATATCATTT
 TTTAAACAAAACCTAAGAACAGCCAGTCAGTTAGCTAAACCAAAATATTGATTATG

FIGURE 3X

AAAAGGGTTTGTATATTTACAGGATAAGATAACAATAAATTCACTTCAGTCCTTCTTTA
 ATATGTATTTCTGTCCTAACCCAGACACAAAGCAATTAAACTGATCGTCAAGAAA
 TCTGTTTCTCCTACACAATCAATGAAAAGTAATCTAACAGTGTGTCAGGCCAGGCA
 [T, C]

AGTGGCTCACATCTGAGTCCTAGCATTTGGGAGGCCTAGGCAGGTAGATTGCTTGAGC
 CCAGAATTTCAGGACAGCCTGGACAACATGGCAAACCCATCTGTATTAACAAAAAAA
 AAAAAAAAAGACCATATGTCAGTCAGTGGAAAAGTAAATATGTAATAAACACA
 TATGAATAATATTAAGGACCATATTTAAACTGATAATAAATTAAATAATAT
 TATCTACGATAAAATGTTTACTTAAATTTCGTTCTTATCATGCCACACAAAATGGCA

41044 TATGAAAAGGGTTTGTATATTTACAGGATAAGATAACAATAAATTCACTTCAGTCCTTCT
 TTTAATATGTATTTCTGTCCTAACCCAGACACAAAGCAATTAAACTGATCGTCAA
 GAAATCTGTTTCTCCTACACAATCAATGAAAAGTAATCTAACAGTGTGTCAGGCCA
 GGCACAGTGGCTCACATCTGAGTCCTAGCATTTGGGAGGCCTAGGCAGGTAGATTGCT
 TGAGCCAGAATTTCAGGACAGCCTGGACAACATGGCAAACCCATCTGTATTAACAAA
 [A, -]
 AAAAAAAAAGACCATATGTCAGTCAGTGGAAAAGTAAATATGTAATAAA
 CACATATGAATAATATTAAGGACCATATTTAAACTGATAATAAATTAAATA
 ATATTATCTACGATAAAATGTTTACTTAAATTTCGTTCTTATCATGCCACACAAAAT
 GGCAAATGATTAAGAGAGTTGAAAATTATGTTGATAGTGAAGAGGTTGCGGTTA
 AAAAAAAAAGAGAGAGAGAGAGAGAGAAGTATGGGCCATGGGATAGTCTGTAAATCA

41311 GACAACATGGCGAAACCCATCTGTATTAAAAAAAAAAAAAGACCATATGTCG
 CAGTCAGATGGAAAAGTAAATATGTAATAAACACATATGAATAATATTAAGGACCAT
 ATTTAAATAACTGATAATAAAATTAAATAATATTACGATAAAATGTTTAC
 TTAAATTTCGTTCTTATCATGCCACACAAAATGGCAAATGATTAAGAGAGTTGCAA
 AATTATGTTGATAGTGAAGAGGTTGCGGTTAAAAAAAAAGAGAGAGAGAGAG
 [-, G, A]
 AGTATGGGCCATGGGATAGTCCTGTAATCAGTCACCTGAACCACTTTAATACTCAA
 AAGACTTATGAGAATAAAATCTGATTTGCTAAGATTATTAGCAAATAATCTTAC
 TCCTCTGTCCTCTAATTATCCTCAGCTTGACCATGTATGAAAGAAAATTACAT
 TTCAGTGTAACTATTTAAAGATGAACATTCCATTAAATCAGGATGCACCTTATAA
 TCAGTAGCATCTAACATATAAGTCAGGCCAGGCTGCAGTTGACTGTAGTTAGAATTGC

41313 CAACATGGCGAAACCCATCTGTATTAAAAAAAAAAAAAGACCATATGTCGCA
 GTCAGATGGAAAAGTAAATATGTAATAAACACATATGAATAATATTAAGGACCATAT
 TTTAAATAACTGATAATAAAATTAAATAATATTACGATAAAATGTTTACTT
 AAATTTCGTTCTTATCATGCCACACAAAATGGCAAATGATTAAGAGAGTTGCAA
 TTATGTTGATAGTGAAGAGGTTGCGGTTAAAAAAAAAGAGAGAGAGAGAG
 [-, A, G]
 TATGGGCCATGGGATAGTCCTGTAATCAGTCACCTGAACCACTTTAATACTCAAA
 GACTTATGAGAATAAAATCTGATTTGCTAAGATTATTAGCAAATAATCTTAC
 CTCTGTCCTCTAATTATCCTCAGCTTGACCATGTATGAAAGAAAATTACATT
 CACTGTTAATCTATTAAAGATGAACATTCCATTAAATCAGGATGCACCTTATAATC
 AGTAGCATCTAACATATAAGTCAGGCCAGGCTGCAGTTGACTGTAGTTAGAATTGCAC

44701 TCTAAAAACTTCTGCAAGACAGAGCAATGCTATCTCACATTATGTTATTGGGTGCTA
 TAACATCATCTAACGCTGGAGACAGCCTACTGTCATAGCTTGGAGTCCAAAGACCTGGGT
 TTGAATTCTAACCATTTCTAGCTAAATGAACATGGCAAGTTATGATGTCCTCTGAAC
 TTTCGTTCTTGTCTGTAATGGCAACAATGATAATAAGGACTTTCTAATTCTTATT
 GAGAATTCATAAAACAAATGCATAACAAGCTCCATGCACCATAAATGCTCAATAGATG
 [C, A]
 TTGCTTCTCTGTCCTGCCCACACAAATTGTTGACAGATGTTCAATAACCTAACTGCTAG
 CAAGTATTACCTGAAATTAAACCGATTGTTCTTCACTTAGCAGTATTATTCT
 TGTCCACAATAGAGGAAGCACAATTGCAAGTTCTGATGCTGCAATGACCTTTATACATT
 GAAGAGTTTCTGGTCATTAATCAGGAAACAAACTTACTCACCATAATGAGGCGA
 GTAACTCTACAAGACTCTACAAGGTCTGTAAGAAGCTATAAGCCAAGGGGGAAAAAAA

46020 AAATTCAAAATAACATTAAATATGACACTATCTTGAATGACCACACAATTAAA
 AAGCAATCATTTACGGTTCTTGTAGTCAGTTAGCACAGCACACTAGAAATCATAGAAT
 AAAGTGAAGCAAGATGCTCTAACAGCCTGATCACTTTAGGACTCACATGGCTAGGT

FIGURE 3Y

ACTATGCTGGAAAGAGAAAAATAATAATTTCTAACCTGCTTGAGACATAGTGGTATAA
 ATGATAACACAGCTGCTAACGTGATGACTTCACATTGTCGCAGAGCAAGAAACTA
 [T, C]
 AGATGCAGTAACAAAAGCTCATTCAATGAACATGGGACTGTAGATAACAAACTAAC
 TCA
 TTTCTTGGGTACATGCCCTGATTGGGATTGCTGGATCATATGGTAGTTCCATTAA
 TATTTGAGGAACCTCCATACCACATCTTCATAATGGCTGTGCTATTGATGCCAC
 CAGTGTGCAAATGCTCCCTTCCTCCACATTCTGCCAACACCTCTTCATCTTTGAT
 AATAGTTATGAGGAATATCTCACCATGGCCTAGACTTCATTGCTGTGACTAATGA
 46036 TTTAAAATATGACATACTATCTTGAATGACCACACAATTAAAAAGCAATCATTACG
 GTTCTTTAGTGTTCAGTTAGCACAGCACTTAGAAATCATAGAATAAAGTGAGCAAGATGC
 TTCTCAAAGCCTGATCACTCTTAGGACTCACAATGGCTAGGTACTATGCTGGAAAGAG
 AAAAATAATAATTCTAACCTGCTTGAGACATAGTGGTATAAATGATAACACAGCTGC
 TGAAACGTGATGACTTCACATTGTCGCAGAGCAAGAAACTATAGATGCAGTAACAAA
 [A, G]
 CTGCATTCAATGAACATGGGACTGTAGATAACAAACTAACATTCAATTCTTGGTACATG
 CCCTGTATTGGGATTGCTGGATCATATGGTAGTTCCATTAAATATTGAGGAACCTC
 CATACCACATTCCATAATGGCTGTGCTATTGATGCCACCATCAGTGTGCAAATGCTC
 CCTTCTCCACATTCTGCCAACACCTCTTCATCTTTGATAATAGTTATGAGGCAA
 TATCTCACCATGGCCTAGACTTCATTGCTGTGACTAATGATATTGAGCATTTC
 46095 GGTTCTTTAGTGTTCAGTTAGCACAGCACTTAGAAATCATAGAATAAAGTGAGCAAGATG
 CTTCTCAAAGCCTGATCACTCTTAGGACTCACAATGGCTAGGTACTATGCTGGAAAGA
 GAAAAAATAATAATTCTAACCTGCTTGAGACATAGTGGTATAAATGATAACACAGCTG
 CTGAACGTGATGACTTCACCTTGTCCGCAGAGCAAGAAACTATAGATGCAGTAACAA
 AACTGCATTCAATGAACATGGGACTGTAGATAACAAACTAACATTCAATTCTTGGTACA
 [T, A]
 GCCCTGTATTGGGATTGCTGGATCATATGGTAGTTCCATTAAATATTGAGGAACCT
 CCATACCACATTCCATAATGGCTGTGCTATTGATGCCACCATCAGTGTGCAAATGCT
 CCTTCTCCACATTCTGCCAACACCTCTTCATCTTTGATAATAGTTATGAGGCAA
 ATATCTCACCATGGCCTAGACTTCATTGCTGTGACTAATGATATTGAGCATTTC
 CATATATCTTGGCATTGGTAGGTATCTTGTGAGAAATGTGATTGAGGTTCTTAGT
 47608 GTTAGCCAGGCTGATCTCGAACTCTGCACTCTGGTGATCCACCTGCCTCAGCCTCCAA
 AGTGCTGAGATTACAGGCGTGAGCCACCGTGCCCCGCCCTTGCCCCTGTAAATGGGG
 TTGTCTCTTGCTATTGAGTTCTTATATATTGAGGTTCTCTTCACTCTAAATGATTGTTCTT
 GGCTTCAAATATTCTCCATCGTAGGTTGTCTCTTCACTCTAAATGATTGTTCTT
 GCTCTGAAGACACTTTAGTTATTGAGGTTCTTCACTCTTAGGAATAAAACACATTGAGAAGTCTGA
 GTCTCTATTAACTATTCTGAAGTGCCTGTAGTGTGTTACATCTAAATAATA
 51949 TTTAAAATGTGATTAAGAAGAGAATAAAATACATAGGGAGCTGGGACTCTTTCTTAT
 TTTCTTTAGCATCCAATACTTTGCTTACAGCTATCCATAGGGATCTGGCATCTTGAACC
 ACCAGGATTATGAAAGCCCTACAGCAAGCTAAAGACTAACTGTAAAGTCTTCACTGC
 TTGTAATGGTTATATCTATTGCTAAAGGCCCTAAATATCATTTGCAAATAGTTATGA
 TTCTAATCTTCTAGAGTTAACACGTGAGAAAATGCTACTCTGGTCACAGGA
 [-, C]
 TTAGAAATAGTGCCTATTCTTCTGGCTGAGATAGAGAAAAAGAACAAAGTTCTGTGG
 AGCCGTGGTCCAGTCTGCAAATTGCTCTATCTCAGTTGCCATGGTTCCAGGAGAACG
 TGGCTCTCATCTTCTGCCCTGCTGTACTCTCCCTGTCACCTGTTCTATTT
 CCCTCAGCTTCTAACTGAGGATGCCAGCAGAAGTTAGAGTCACAGATGGATTGAGGA
 AACAAATTGGATGATGCCAACAAAGCTACTGTGGTGGCATATGCTGCTCCCCAAC
 52150 TGCTAAAAGGCCCTAAATATCATTTGCAAATAGTTATGATTCTAACTATTCTAGAG
 TTTAACACGTGAGAAAATGCTACTCTGGTCACAGGACTTAGAATAGTGCCTATTCC
 ATTGGTCTGAGATAGAGAAAAAGAACAAAGTTCTGTGGAGCCGTGGCCAGTCTGCAA
 ATTGCTCTATCTCAGTTGCCATGGTTCCAGGAGAACAGTGGCTCTCATCTTCTG

FIGURE 3Z

CCTGCCTGTACTTCTCCCTGCCACTCTGTTCTCTATTTCCCTCAGCTTCCTAAGTGAG
 [G,A]
 ATGCCAGCAGAAGTTAGAGTCACAGATGGATTGAGGAAACAATTGGATGATGCCAT
 ACAAAAGCTACTGTGGTGGGCATATGCTGCTCCCCAACTTCAGACATTGGGTTCAAG
 TTGGTCAGGCAATCAACAGTGATCCTAACAAAATGTCTGGTGGAGAGCAATAATCA
 AGAAAATTGGCCAAGTGCTCCCTGCCAGATTGTGCTTAATAAGATAACTGGGTTCC
 AATAAAACAGAGAAAATATGTTACATTAAAAAATTCTGTTGTTCAAAACAATGTG

52426 TTTTCCCTCAGCTTCTAACGTAGGATGCCAGCAGAAGTTAGAGTCACAGATGGATTGT
 AGGAAACAATTGGATGATGCCAATACAAAGCTACTGTGGTGGGCATATGCTGCTCCCC
 AAACCTCAGACATTGGGTTTCAGGTTGGTCCAGGCAATCACAGTGATCCTAACAA
 AATGTCTTGGTGGAGAGCAATAATCAAGAAAATTGGCCAAGTGCTCCCTGCCAGATTGT
 GTGCTTAATAAGATAACTGGGTTCCAATAAAACAGAGAAAATATGTTACATTAAAAA
 [-,T]
 TTTCTGTTGTTCAAACAAATGTGCAAGTTTCTATATAAGAAGAAAAGTCTCCAGGCC
 AACATCATAGGGCTCATCATCATTGTTTCTTTAAGTTTCAATTAAATCCAATA
 AGTCAAAATTTCAGGTACCTACTATCTGCCAGGTGCTGCGCTGGGCTACA
 CAGATGGAGGGGTGCAATTGGATCTCTAGTGTGTTGGGTTGGATTCTACCCACA
 CTCTTCAACCAGTTCTCTTGTACTGGGTTGCTATTGTGAGCCCTGCTTCATGGCT

Additional SNPs 3' of the ORF (DNA positions refer to the genomic sequence provided in U.S. Serial No. 60/265,151, Attorney Docket No. CL001098-PROV, filed January 31, 2001):

56707 CTGCCAAGATCGATGCTGGGTGGAGTAGCCCGATTCTACAGATGAGGAAACAGAGGCTTT
 CTCCCTAGGCTCACAGAGAGGTGTATACTTATTGGAATGGCTGAAATCTGCATCCAAACC
 TTGTTCTCCTTCATTAATCATGTTGATCCCTCTGCTCATTTGAGGATGAGTCTGA
 AAAATAAATTATATTGAATTGCACTCTGCTATAGTGCTAACATTAGTAGGTACTCAATA
 AAAGTTCCCATTCAAGTTTTTTGTTGGTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 [-,T]
 TTTAGATGAAGTCTCAATTGTCACCCAGGCTGGAGTGCACTGGCATGATCTGGCTCACC
 GCAGCCTCCGCCCTCTGGGATAAGCGTTCTCTGCTTCAGCCTCCCGAGTAGGTGGGA
 ATACAGCGCACGCCACTGAACCCAGCTAACATTGTTGATTTTAGTAGAGACAGGGTTTC
 ACCATGTTGGCTAGGCTGGTCTCGAACCTCTGACCTCAAGTGATCTACCTGCCAGCCT
 CCCAAAGTGTGGATTACAGGTGTGAGCCACTGCCATTGGTTTTACACAGTGT

57444 CTTTTGTTTACTTGATGCCCTAACCTTGCTGAATCCGACATCTAACAGAGCTGAC
 TCTGAGTTTCAAATGCCACTTAAGTCAGTTGTGCCCCGTTAAGGCTGTTCTATTG
 GTGATGGGTCCATTCTGCTCCCCACACCTAGACTGCACTAACATTGCTGCTG
 CCCACAGGGCCTTCCCTGGAGAACCTTGATCTACATGCTACATAATGGGTATCCA
 GTAAGGGCTACTAAATCACAGACAACATTAGTGTACATTGTTAACATTGTTAAC
 [A,G]
 GTATAGTGGAAAGAGTGTGAAGTTTCTACAGAGCACACCTGACCACTCTAGTGCTTC
 TAGTATTTCACACAAGCCCCCTACCTGGCACATAATAAGTAGTCAGTAGATATTGTA
 ATGAAATCAATGACTAACAGAGTTAGAAAACCTGAGTTCTAGTCCAAATTGCA
 ACCCTCTGGACTCTAAATAATTCTTATTGCTGCTTGGCAAGAAGAACATGTAAGTT
 ATTACCTTAATAATTGGTAATAATAATTGAGGACTAACATGAGCTAGACACTTACAT
 ATTACTT

58021 CTAGACACTTACATATTAACTTACTTTGATTACAACAGCCTTATCAGATAGAGACA
 ATGTTGAAACCCACTTACTGATGAGAGAGCTGAGGCTTTGAGAGAGGTATGTGACTT
 GCTTAGGGTCACCTAACAGGAAGGGGGTGACCTAGAAATTCACACCTGTTGGACTCCA
 AGTGGGTGCTAGCGTATTCCACTTACCTTAATTATCAAAGGGCAGATATAATGATTG
 GTAATTAAAACAGTGCCTAGACTGGGACTGGCATAAACCTTGCAAGGTTCTTCCA
 [A,G]
 ATGATTATGTCTTCCACCCAGACGTGATTTAGAATCTGTGAGCCTGGCAGATATTTC
 AGGAGTGTAAATCTGAGTGGAGTTCTACCCCTGGGACTCCAGCAGCCTCCCTGCTACAGC
 TAATGAAGCCACTGGCGTTACTGAATCTATGAACCTCGATTGGGCTCATTACTGTCTCA
 CTTCTGGAGCGTGTGAAAGCTCCTGGGGAGTTACTATTAAACATCTTTATTAAACCGTC
 CCCAAATCAAGTCAGTGAACATTAAATTAGATACACAGCCACTTGTGATCTTCAATTGGT

58064 CTTATCAGATAGAGACAATGTTGAAACCCACTTACTGATGAGAGAGCTGAGGCTTTG

FIGURE 3AA

AGAGAGGTATGTGACTTGCTTAGGGCACCTAACCAAGGAAGGGGGTACCTAGAATATCC
 ACACCTGTTGGACTCCAAGTGGTCGTAGCCGTATTCACTTACCTTAATTATCAAAGG
 GCAGATATAATGATTGGTAATTAAAACAGTGCCTAGACTGGGACTGCCATAAACTT
 TTGCAGGTTCACTTCAAAATGATTATGTTCTACCCAGACGTGATTAGAATCTGTG
 [A, C]
 GCCTGGCGACATATTCAGGAGTGTAACTGAGTGGAGTTCTACCTGGACTCCAGCA
 GCCTCCCTCGCTACAGCTAATGAAGGCCACTGGCCTACTGAATCTATGAACCTGATTG
 GGCTCATTACTGTCTCACTTCTGGAGCGCTGCTGAAAGCTCTGGGAGTTACTATTAAC
 ATCTTTATTAAACCGTCCCCAAATCAGTCAGTGAAATTAAATTAGATAACACAGCCACTT
 TGATCTTCATTAATGGTTGCTTCTAGTTCTACATTTATTTAGTTAGTTCTCATCTTAA

59067 CTGTAATCCCACCACTTGGGAGGCCAGGCAGGGGGTTCACTTGAGATCAGGAGTTCGA
 GATCAGCCTGGCAACATGGTAAACCCCTGTCTACTAAAAAATACAAAAATTAGCCAGG
 TGTGGTGGCAGGCACCTGTAATCCCAGTACTCAGGAGACTGAGGCAGGAGAATCACTTG
 AACCCAGGAGGCAGGGCTGAGTGAAGCAAGATCATGCCGTGACTCTAGCCTGGCA
 ACAGAGTGAAGATTCATCTAGAAAAACAACAACAACAAAAGAAACACACATAAAACA
 [T, C, G]
 AGCAGGTATACAAGTGGCTCACCTGAGTTACTTTAACGTTAAAGTAAGGTTAATA
 TATTATTTCACTTTTATTTTCACTCAACCCTACTTCTTATTATTCAGCAAATATG
 TATTGAATGCTAGGTACTAGGGACTGAGAGAGTAAAAAATAAATGACACTGGTACCTG
 CCTTCCAGGAATATAGTCTAGAGGGAAAATAATAATAACATGTGGAAAGTATAC
 TACAGCAGCATTGCCCTGGGATCTTAAGAAACGAGGGAAATCTGGACTTGCTGTGAT

60034 AGCCACCGTGCCTGCCCTAGGGATGGTTAAAGAAAGAGATGTGAGCTGGCCTCCCA
 AAGTGCAGGGATTACAGGCATGAGCCACTGTGCCCGCCACCCCTGCTATTAAATCAA
 GGAAACAGAACAGGGGAAGGAACAGATTATAGAGAAGGTAATGAGTATAAGGTTAAACA
 TTTGAGATTAAAGGTATCTGGAACCAACAAATGGAGATATCTAAAAGCAAGTAGAAA
 TATAAACTGTGAGTACAAAAGTCCAGCCTAGAAATACAGAAGTCACATGCTTAAATCGGT
 [A, G]
 TTTAAAGCCTCAGGTGTGAATTAGTTGCCAAAGGGAGAGAGTGTAGAGAAAGAAAG
 GACAATGAGGGAAACCCCTGTGGGCCAGTACTGCAGGACTGGTAGAGGGAAAGGGAGTCTT
 TAGAAGCTGAGGAAACAGCCAGAGGAGCTAAGGGAGACTAGTAGGTAACTCTAGCAAT
 ACCATGAAATCATATGCCAGCACTCACTGGAAAGAGGCTGGTTCCATGCCGTGTAT
 TCTCAATGCTGAGCTCATTGGCTGCATGTGGTGGCCCTCAATATTGTGGAGACTACAA

63709 TACTTCAACCCATGCAGTAGAAACTATTACTATCCCTCTTGCAAGGTGGAAAAC
 TGAGGCCAGTGGTTAACGAAATATCTCCGGTCACACAGCTGGTAAGAGGCATAGTGT
 GGGTTACCCGGGTCTGGGTCAGTGCCTGGCCACGCATTGTTACTGCCCCATAAC
 TTTCAAGGAAGGGAAAGAGGAAGGAAAAGCAGATAGGATTATTGTTAATGGTCC
 AGAGCAGGCATTGGCACTCATTATTCATTGGTGCCTCAGGTGAATACCACCTCAA
 [A, T]
 TTGCAATTGAGAAAATGAGGGTTGCCCTACAGAATGCGAGAAAATTGCAATCTACT
 CATCTGACAAGGGCTAATATCCAGAACACTAACAGAACTTAATAAGTTACAAAAAAA
 AAAACCATCAAAAGTAGGCAAGGATATGAACAGACACTCTCAAAGAAGACATTAA
 TGCAGCCAACAGACACATGAAAATGTCATCATCACTGGTCATCAGAGAAATGCAAAT
 CAAAACCAATGAGATACCATCTCCACCAAGTTAGAATGCAATCATTAAAAGTCAGG

63817 GAGGCATAGTGTGGTTCACCCGGGTCTGGGTCAGTGCCTGGCCACGCATTGTTAT
 ACTGCCATAACTTCAAGGAAGGGAAAGAGGAAGGAAAAGCAGATAGGATTATT
 GTTTAATGGTCCAGGCAGGGCATTGCACTCATTATTCAATTGGTGCCTCAGGTGAA
 TACCACTTCAATTGCAATTGAGAAAATGAGGGTTGCCCTACAGAATGCGAGAAAATT
 TTGCAATCTACTCATGACAAAGGGCTAATATCCAGAACACTACAAAGAACTTAAATAA
 [G, A]
 TTTACAAAAAAACCATCAAAAGTAGGCAAGGATATGAACAGACACTCTCAA
 AGAAGACATTATGCAAGCCAACAGACACATGAAAATGTCATCATCACTGGTCATCAG
 AGAAATGCAAATCAAAACCAACATGAGATACCATCTCCACCAAGTTAGAATGCAATCAT
 TAAAAGTCAGGAAACAACAAATGCTGGAGAGGATGTGGAGAAAATAGGAATGCTTATACA
 CTGTTGGTGGAGTGTAAACTAGTTCAACCATTGAGAAGACAGTGTGGCATTCTCAA

64845 TAGGAGAAATAGCTAATGTAATGATGAGTTAATGGGTGCAGCAAACCAACATGGCGAT
 GTACCTGTGTAACAAACCTGCAGGTTGACCTGTACCTAGAACCTAAAGTACAAT

FIGURE 3BB

AATGAAAAAAATTAAATTAAAAAATCAGAAAAAAAAGAAAGAAAATGAGGGTTGCCA
 TGGATGGTCAAAGTATCTTACATGAGGTCTCAGCAAAACTGAAGCAGCAGACTGTATT
 GAAACCCTAACGCTAACCCCCAACCGTGCCACAAGAACCCACTCAAGTTAGAA
 [A, -]
 GAGTATTAAAATATTGGAGGCCAAAACACAGCACATAGACCTCTCAGAAGGGAAAATA
 GAAAATGGGAAAGGATGGAATGGATTTCATTTTGTGATTGAAATTGGGAGATGACTGA
 ATGAGGAAATATTTGATTTGTTGCCAGGGAGAGCTGAAATAGGCAGCAGAAAGT
 GGTTGAAGAGAAACATACTAAACAAATGCCAGATATTCTTATCTTACTGGTTATTTG
 AACTTAGGCAAAATCATACTGAACAGAGAGTAAATAACCTGTATAGACAATTGCTCTCT
 64848 GAGAAATAGCTAATGTAATGATGAGTTAATGGGTGCAGCAAACCAACATGGCGATGTA
 TACCTGTGTAACAAACCTGCAGGTTGTGCACCTGTACCTCTAGAACTTAAAGTACAATAAT
 GAAAAAAATTAAATTAAAAAATCAGAAAAAAAAGAAAGAAAACGAGGGTTGCCATGG
 ATGGTCAAAGTATCTTACATGAGGTCTCAGCAAAACTGAAGCAGCAGAGTCTGTATTGAA
 ACCCTAACGCTAACCCCCAACCGTGCCACAAGAACCCACTCAAGTTAGAAAGA
 [G, -]
 TATTAAAATATTGGAGGCCAAAACACAGCACATAGACCTCTCAGAAGGGAAAATAGAA
 AATGGGAAAGGATGGAATGGATTTCATTTGTGATTGAAATTGGGAGATGACTGAATG
 AGGAAATATTTGATTTGTTGCCAGGGAGAGCTGAAATAGGCAGCAGAAAGTGGT
 TTGAAGAGAAACATACTAAACAAATGCCAGATATTCTTATCTTACTGGTTATTTGAAC
 TTAGGCAAAATCATACTGAACAGAGAGTAAATAACCTGTATAGACAATTGCTCTCT
 64914 TGTAACAAACCTGCAGGTTGTGCACCTGTACCTCTAGAACTTAAAGTACAATAATGAAAAA
 AATTAAATTAAAAAATCAGAAAAAAAAGAAAGAAAACGAGGGTTGCCATGGATGGTC
 AAAGTATCTTACATGAGGTCTCAGCAAAACTGAAGCAGCAGAGTCTGTATTGAAACCTA
 AGTCAGCTAACCCCCAACCGTGCCACAAGAACCCACTCAAGTTAGAAAGAGTATTA
 AAATTTGGAGGCCAAAACACAGCACATAGACCTCTCAGAAGGGAAAATAGAAATGG
 [G, T]
 AAAGGATGGAATGGATTTCATTTGTGATTGAAATTGGGAGATGACTGAATGAGGAAA
 TATTTGATTTGTTGCCAGGGAGAGCTGAAATAGGCAGCAGAAAGTGGTTGAAG
 AGAAACATACTAAACAAATGCCAGATATTCTTATCTTACTGGTTATTTGAACCTAGGC
 AAAATCATACTGAACAGAGAGTAAATAACCTGTATAGACAATTGCTCTTAGGCCA
 CCTGGACTATAAAATGCCAGCAGAGAGTCCACATTGATTGCGCTGACCTTGAAAC
 67367 AGGAGGATGTGAGTCAAATTGCAATTAGGGCCCACCTAATGCTTCATCTTAACTAATTA
 CATCTACAATGACCTTATTCATATAAGATCATATTCTAAAGTAATTGGGTTAGGACT
 TCAACATGTGAATTGGGAGCACATAATTCAACCCATAATAGTGCACCTTACCAAATC
 ATAAAAATTATCATCAGGAGATGAGGCTTAAACATTACATTAGCCTACCTGATACTGAAT
 CATTTTAAACCAAGCCAAGAAGAGCATTAGAATTAAACAGTATATTAAACAGTATATTGGCAACAG
 [G, A]
 GTTTTGGGTTGGATTTATTTTAACGCCCTGTATGCTTCCCAGAATGGTCCCACT
 GCCTACGCCCTCGAAGCCTTATGTTGCTGGAACAGGTGAGTACTACCTCAGGAAGGGAT
 CTTTAAGGGTTCTTAAGCAGGATTGGAGAGACATTCCCTGGATCTCAGTCCACTGAAC
 AGCAGCCCCGAGCACTTCCATGTGGGGCTCTAAGCTGTAGGAAGATGCCCTCTGCAAGC
 GCCAGACCCCTGAGAGTCTGTTAATTCTATGAACCATTACTTCAGTGAAGT
 67497 AATTTTGGGAGCACATAATTCAACCCATAATAGTGCACCTTCACCAATCATAAAAATT
 ATCAGGAGATGAGGCTTAAACATCACATTAGCCTACCTGATACTTGAATCATTTTTTA
 AACCAAGCCAAGAAGAGCATTAGAATTAAACAGTATATTGGCAACAGGGTTTCGGG
 TGGATTTATTTTAACGCCCTGTATGCTTCCCAGAATGGTCCCACTGCCTACGCC
 TCGAAGCCTTATGTTGCTGGAACAGGTGAGTACTACCTCAGGAAGGGATCTTAAGGG
 [T, A]
 TCTTTAAGCAGGATTGGAGAGACATTCCCTGGATCTCAGTCCACTGAACAGCAGCCCC
 GAGCACTTCCATGTGGGGCTCTAAGCTGTAGGAAGATGCCCTGCAAGGCCAGACCC
 TGAGAGTCTGTTAATTCTATGAACCATTCTACTTCAAGTGTAGTTGGTCGTTAAA
 ATTGTTTGTGTCCTCAGCCATGCCCAAGGCCCTGAGAACAGGAGGAGTGTGGTCTGCA
 AGAAAACCTAGTGGTTTATTCTGTACACAGAGAAACCAATAACATCATTGAGTG
 68252 GGGAAATAGTTAGCTAACTAAGCTGTGCCAGGCAACCTCCGGGCTAAGAAGAAACTCAGTGT
 TTTGGGACAATGACCAATTACAATAACCAATTGATCTGAGAGTAATTAGCCGAG
 GCTCTGTTCTTTGCTTCAGTGTAGGAGGCCAAAGGGCAATGAGGAAACATCAGAGAC

FIGURE 3CC

AGGGGAAACGAGCTCAAATGTCAGAGAAAAACACAGTCTTGCAGGTGGGGAGAAGTGGAA
 GAGTTTCACTGGCCAAGATCCTGACTGAACACTCGAACATTGTTTCCCTGAAAATATG
 [G, -]
 TAGAATTAACTTAACCAAAGTTGTTGAATTCTTCACTCTTACTGTTCATTCCTTTA
 AAAAGCTCCACGTAGAATAAAATATCAGGGTACAAAGAGTAAAATAGGTTAGGAACATA
 GAACATATGGACTACCAGAGATCTTCACTGGGAGGGACAGGTATCTCAGGACATCTGCA
 CCCTCCACTCTTATTTCAACAGCACTGTATAACCTGAAACCTTTGGAGACAGGTTCTA
 GGGAACTACTGTTTCACTTCATTCAAGACGTGAGTACAGTCAGGCTCCTCCCTCT
 68580 TGAATTCTTCACTTTACTGTTCATTCCTTAAAAAGCCTCCACGTAGAATAAAATATC
 AGGGTACAAGAGTAAAATAGGTTAGGAACATAGAACATGGACTACCAAGAGATCTTCA
 CTGGGAGGGACAGGTATCTCAGGACATCTGCACCCCTCACTTATTTCAACAGCACT
 GTATAACCTGAAACCTTTGGAGACAGGTTCTAGGAAACTACTGTTTACACTTCATTCA
 AGACGTGAGTACAGTCAGGCTCCTCCCTACCTAGAGATATGTGGATTTAGCATG
 [C, G]
 CCCGTGGCTTCTTCATGTCACTATCAGCTTCAAAGTAATGGCAACTCTCACCTGA
 GAACCATCTTAATACTCCATGCTGCTGCTGAGCTGCCCTGTCCATGGCAGAAGA
 TAGTTCACCAAGCCTCTGCTATCACCCACCAGCCTTCTTGAGGGCTGAGCAAGGCT
 TGAATTCTCTGAATACCTCTGGCTTCTGACGATATAGCACCCATGGCCTCTGCGCC
 TTCCCTGTCCCCTAGCAATATGTATTCACCTTCTCAGACTCTGGCTCTGCTCA
 69990 CTGTGGATTGGCTGTTGAATCAGGTTGAGATGTGGGAGTAACAAGCAGCCGAAGTGT
 CACTGGCTTCTACACAATCCCTCAGAGGTGAGTGGACATTACAGGCCCTGTAGA
 TGAATCCCCGGGGCTGCTTGAGGTTGATGGTGTCTCCTTAATGTGGGCTAGTAGGT
 ACGCACTCACTTTAGATTGGCAAATTGAGGACAGCTCTGCAATGTTCTTCC
 TAGTATTGGATGTATTCTGACTGTGGCATCTACTACATCCAAACTGAGAACATTAA
 [G, A]
 AAGTGCTACTCTATCCCTGCCCTGTTCTTCTGTAGGCTAGGGGGAAAACCAAAG
 AACCCAGTTGAGCTCATACTGACCAGCCTGCTGCACCTCAGAGGTGAGTGGCAGTGC
 GTGGGGAGACTTTATACTCAGAGCCAGGCTGCTAGGAAATCAAACACTGCTGTCC
 CAGACCCCTGAGAACAAACCAGATTAGTAGTATGGAGTGTGGTTAGATGGTGT
 TTACGCAGTCACAAACTCAATTCTATTGTTGTGTTCTATTCTGGAC
 71472 TAGTTAACATCACAAACCTAACAGAGTATGAAATTACATTTACCTGGAAAGGTGCTGGTAG
 GCAAATTAAACATTGTGATGTTCATTTTATGCCATGTTATTTAAAGTAGGGGT
 TGTAACCAAGTGGATAATTGTCAGCAGGAGTTAGGGTGGCCACATGTACAACAT
 GACAGTAAAGGCAATTGTAACAAGCAAGGCCATAGGTGACAGGAAAAGCATAATGATA
 CAAACACGGAAGATGTCACTAACATTGTGCCAAAAAGTAACATTGTTCC
 [A, G]
 GGACTCTTCTCAGCCTTGCACAAAGAGCTCAATGTGCGATAGCAAGGCCGATTACT
 GGGGACTTGCCAAAGGCCAGATCCTAATGGTCTGCTACAGGTGCTGAGGT
 TTGTGTTCATGTGGGTGGAGTTGGCTTGACAGGGAGACGACACACTTGGCTCCT
 AGGAGGAAGAGACCTTCACTTGCCCACTTGCCCTGGTACCCACCTCTACCGCGAAGGAG
 AAGGAGAACAGCAAGTGCAGCAGTCAGTTACAGGGCTGTGAGACTGGAACAAAGTCCAGA
 71664 AATTGGTAACAAGCAAGGCCATAGGTGACAGGAAAAAGCATAATGATAACAAACCGGAAG
 ATGTCAGTAAATCAACATTGTGCCAAAAAGTAACATTGTTTCCAGGACTCTTCC
 TCAGCCTTGCAAAAGAGCTCAATGTGCGATAGCAAGGCCGATTACTGGGCACTTGC
 CAAAGGCCAGATCCTAATGGTCTGCTACAGGTGCTGCCAGTGAAGGTTGTGTTCATG
 TGGGGTGGAGTTGGCTTGACAGGGAGACGACACACTTGGCTCTAGGAGGAAGAG
 [T, A]
 CTTCACTTGCCCACTTGCCCTGGTACCCACCTTACCGCGAAGGGAGAAGGAGAAGCAA
 AGTGCAGCAGTCATAGTTACAGGGCTGTGAGACTGGAACAAGTCCAGAAACCACAGAAG
 CCCTGAAACAAACCCGTGGGGAGGGTAGGGTCTGGTTGAAATGAAAATCC
 TAAAAAAAGAGGTCTTGCACTAATTAGTACCTACCCCTTCTTATTCAATTCACTGGTTT
 AAAAAAAACAAAACAAACCTGTTATTGTTATTGAGACAGGGCTAGTT
 71677 CAAGGCCATAGGTGACAGGAAAAAGCATAATGATAACAAACCGGAAGATGTCA
 AACATTGTGCCAAAAAGTAACATTGTTCCAGGACTCTTCCCTCAGCCTTGCAA
 AAGAGCTCAATGTGCGATAGCAAGGCCGATTACTGGGGCACTTGCCAAAGGCCAGAT
 CCTAATGGTCTGCTACCAAGTGCAGTGAAGGTTGTGTTCATGTGGGTGGAGTTG

FIGURE 3DD

GCTTGTACAGGGAGACCGACACACACTGGCTCTAGGAGGAAGAGACTTCACTTGCC
 [A, G]
 CTTTGCCTGGTGACCACCTCTACCGGCGAAGGAGAAGGAGAACAAAGTGCAGCAGTCA
 TAGTTCAGAGGCTGTGAGACTGGAACAAGTCCAGAAACCACCGAGAACCCCTGAAACAAACC
 CTGTGGGAGGGTAGGGTAGGTTCTGTTGGTTGAAATGAAAATCCTAAAAAGAGGTC
 CTTGCACTAATTAGTACCTACCCCTTCTTTATTCAACCTGGTTAAAAAAACAAAAA
 ACAAAAACCTGTTCTTATTTTATTTTGAGACAGGGTAGTTCTGTCACCCAGGCTA

72590 TCTTGGCTTCCCCAGACACTCTACACAAACACAGTCTAAATAAAAACAATATGCCGCCA
 TGCTAACACAAGTTAAAACAGGTCTCCAGCCTCCCTGTCCTGTCCTGAGCAGCCCC
 TCAGCCCTCACTACAGGGCAGTTCAGGAGCCATCTGTTGGTTAATGCTGGGGAGTA
 TTCGAGAGAACAAATCGTGTGGGGGGACTGTGGAGGTGAAAGTTGATAGATGCAT
 TGCTCCCCACCACCTACCCGCCCTCCCCATGTCCAGAAGTTCATATTAACCAGAACAGCA
 [T, C]
 GAAGCTGCAGAACAGTGGATTCAAGGGCAAATTGGCACAAACCTCACCTCACTACCCA
 ATAGTGTGGGTGGACAGCTAAATTGTTCATGAGATTCCCCTGAGTCTCCTTCAGA
 GAGATCCTAGGCTCTAGTGTGTTACTAACATTCTCTTCAAACGTCCTGAGTGG
 CCCTAAAAACCTCTGCCTGGACAGGATACCCCTGGATGAGGAATATCTGCCAGTCCTT
 CTCAGGCCACAGAACATGAGTAGACTTCTACACAATTCTTTCTCTCTAACTGGCCTG

72757 TGCTGGGGAGTATCGAGAGAACAAATCGCTGATTGGGTGGACTGTGGAGGTGGAAG
 TTGATAGATGCATTGCTCCCCACCACCTACCCGCCCTCCCATGTCCAGAACAGTTCATATT
 TAACCAGAACAGCATGAAGCCTGCAGAACAGTGGATTCAAGGGCAAATTGGCACAAACTT
 CACCTCACTACCCAAATAGTGTGGGTGGACAGCTAAATTGTTCATGAGATTCCCCTG
 AGTCTCCTCCAGAGAGATCTAGGCTCTAGTGTGTTACTAACATTCTCTTCAC
 [G, C]
 TCCATTTCATGGGCCCTAAAAAACCTCTGCCTGGACAGGATACCCCTGGATGAGGAATATA
 TCTGCCAGTCCTCTTCAGGCCACAGAACATGAGTAGACTTCTACACAAATTCTTTCT
 CCTAACTGGCCTGAAATTGCAAGGATTGGAAATTGCAAAATTCTCTATCTGC
 CTATGAAGCAATTATTCTGAGTTGAAAGTAGTTATCTGTTGCAGAACAGTTCATG
 TCTTGGGAATCAAATAGCTCAAATTGCAAAATTGCAATCTATGCAAAATTAGGTAAT

72863 CAGAAGTTCATATTAACCAGAACAGCATGAAGCCTGCAGAACAGTGGATTCAAGGGCAAAT
 TTTGGCACAAACTTCACCTCACTACCCAAATAGTGTGGGTGGACAGCTAAATTGTTCA
 TGAGATTCCCCTGAGTCTCCTCCAGAGAGATCTAGGCTCTAGTGTGTTACTAACAA
 TTCCCTCTCCAAACGTCCTACCATGGGCCCTAAAAACCTCTGCCTGGACAGGATACCC
 TGGATGAGGAATATCTGCAGTCCTCTCAGGCCACAGAACATGAGTAGACTTAC
 [A, C]
 CAATTCTTTCTCTAACTGGCCTGAAATTGCAAGGATTGGAAATTGCAAAATT
 CTTCTCTATCTTGCTATGAAGCAATTATTCTGAGTTGAAAGTAGTTATCTGTTGCA
 GAAACAGTTCATGTCTGGAAATCAAATAGCTCAAATTGCAAAATTCTATGCA
 AAAATTAGTAAATTAGAATTCTGGCCAAGACTCCAGCATCTGCATCATGGCACCT
 GGAAGGGAATAATCTGATCTTCTGCTTAAGTCAGTAGGTGTATTGACATTAAG

74565 AAGATCAACTTGAGGATTGTCTTACTGTGATTAACTTAATTCTCTCTTCC
 TGCTCCATCTCAAGGGAACCAAGAGAGCTCTAACTAATAAGACTGGGTGAGCTTCAGA
 AATGCTGCAAACAAGTGTATTCTACCCAAGCTCACCCTCCAGAACATCACCCTTTAGA
 ATTCTGTGCTTTCTCCAGATTCTGTGCTGCCACCCCTGGAGTCCAGAGCCTTG
 AACATGTTTGTGTTGAGACAGAGCTTGTGTTCTGTTGCCAGGCTGGAGTG
 [C, T]
 TGTGGTCAATATTAGCTACTGCAGCCTCTACCTCCAGGTGCAAGTGATTGTCATGCC
 TCAGCCTCTGAGTAGCTGGGATTACAGGTGCACTGCCACCGCCAGCTAATTG
 TTTTAGTAGAGACAGGGTTCGCCATGTTGGCCAGTCTGGCCAAACTCCTGCC
 AGTGAATCTGCCTACCTCAGCTCTCAGAGTCAGTGTGTTGAAATCAGGCC
 TTGGTGGGCTGAGTGTCTCCAAAAGAATCTTGATTATATTCTGTTATAA

74850 GCCCAGGCTGGAGTGCTGTGGTGCAATTAGCTACTGCAGCCTCTACCTCCAGGTG
 AAGTGTGATGCTGCTCAGCCTCTGAGTAGCTGGGATTACAGGTGCACTGCCACCGC
 CCAGCTAATTGTTAGTTAGAGACAGGGTTGCCATGTTGGCCAGTCTGGTCC
 CAAACTCTGGCCTCAAGTGTGATCTGCCTACCTCAGCCTCTCAGAGTCAGTGT
 AATCAGGCCCTACTTGGTGGGCTGAGTGTCTCCAAAAGAATCCTTGATTAT

FIGURE 3EE

	[A, G] TATTTCTGTTATAATTATTTCTGTCTTTATGTGTACATGGTCCCCAGACACACG GTGGAGGGCAAGGGAGCTGAGTGTAGAATGAGGAGATTTTCCCCTCAACTTAGTAAC AGGACAGTCAGTAAGAGTTAGTATGGGGTTACTTTCCAGTTGCCATCAACTTTAGCA ATTCCAGGAAATTCTACTAAAATCTAAGTCTAGCCATCTCCTTTCTTACTTTTG TTTTATCCCTTGTCCCCAGAAGGGAGCTGGAGAAACTCTATTTCTCCAC
75462	GGGCAGGGTTCTGAAGCTGAAGACCTGGCCTCCAGATGCTAAAAGGCTTCCCAGAGA CCGCGTCTCCGCCAGGAAGCACTTGTTCATGATTATTCAGCGCCCTGCCATCTCAGCT GTACCAAGCTTCTGATGGTGAGCGAGGGAGTGTGTGCGTGTGAGTGCATGTGCGTG AGTGCCTGTGTGTAAAGTCTTGGTCTTAAGTAGTTGCCTCAGCACCGGAGAATCAT AGCATTACCCCAAGGAGTGAAGTAGAGATCAGTTGCCTGGGAGAAGCAAGATAGGAC [G, C] TAATCTGTCTGAGTTTGATGAGCTCTCTCAAACACTCTGAAGCACTGGTGGGAGAGG TTACAAGGACCTCTTGTAAATGGTCCAGACATTCACAGGTACACATTACACTCAGAAA TTGGATGAGATGGACCTGTCTCTGAGTTGTTGCCTAGCTACCATCTGCCAGGAAGCC ACACCAAGTGTCTAACAAAGACTCTTCCCTTCTGCCAGAGTAAGATGATAGGTGAA GCAGGATATGCTCTGAGAGGGAGCTGGGCTTCTGATTGGTAATAGCAAGCTGCAGAAG
76045	AATAGCAAGCTGCAGAAGGCAGTGCCTGGGTGCTGGGAGGTCTCC GAGGCTGCCACCTCCTGTAACACACAAGTTACCTTGAATCAGCCTTGTGCGCTGGGC TGAAGTCATCTTCCAACACTGAAATCTGCTGAGGGATCATGTGGTTGAACTCCGTCAT GTTCTTGGACTGTGCCAGGAAGGGCTACAGGAGGATGTGGCGAGTGTGCTATGGGGAC TATCCTAGGTGAGGTTCTTGAAAAAAATCCACCATTCAACTAAAATAGTTTAGGA [A, G] CAAGGGACAAGTAGACAAGAAAAGCAAAGCTACCAAGGAAGGAAAAACAGAAAGAGAGAGAA GCAGCCAGGGTTGTTAGAAGTCCTAACGCCAGAGAAAAGAAAGCTTAGGAGGGAGGGC CTAAGGGCTGAACTGCATGAGGACACTGGAAAGGGCGTGGGGAGTGGCGATGGGTG CAGTGAGATAAGGATGGGACAGGGTGAGGAGCTACTGCCAACAGGTGTGAAACAGCC TGGTCCGCCCTGCCAGAGTTGCAGACGCAGCTCTGTGCTAGGACATCGTCCTGCA
79973	ACTTCAGGCCTTCTTGAGTGTATCTCTTAATATATTGAAAGTCCCTATGATATCAC TTCCCAAAGGCCACTTCTGGCTGAATTCCTTAACCTTGTGTTCAAATACAAATTCTGT TTCTCCACCTTTAGTCATTGTTATTGTTCTCTGTAATCTGTTCAAATTATTT TGCTTATCTCTGAGAATATGGAGGCAGCATAGACTCAAATTCTGATGGTGGAGAAT CATGTTCCATTCTTATTGGAGGTTACTGAGTGTCCATGAGGTGTGATATTAAGGAT [G, A] CAAAAATGAATTAGTCATAGACCCCTGCTCTCAAAGAGCTACGGTCTTTAGGAATAAG ACAAGTATATAAACAGCTGCAGATCAAGTATACAAATAAGTCTAAGTGTGAAAGG AGGTGAGATTAACTCCAGCTGTGGGATCCAGGATGATTTGTGAGTGGCCTTGAAGA TGATGGGTCTGGATGATTGGAGAGGAAGGGCATACGGGCAAAGGAATGCGTGTCT CAATACCATCTAAGATCATTCTGAAGTTGTTCTTTAATCATAGTGGCTCAGCTTA
83181	ATGTATGTGATTGTGCCCTAGTCAGAGTTAAGTGCACCTCGTGTAGTTAGCAACT TCAATTAAAGTGTGTGATCCTCTGGCTTGAAGATATGAATTCTATACATACA CATGAGCTAAATTACCGCATAATCACGGAGATGTGCACTTGAATAATTGAATGAC TAAACATCTCAGCTGATGGATTGATGTGGAGAGTAGTGCAAAACCCACGTGACAC GGAAGATTACAAGACATTGAAATGATAGCTTAATTCAACCTTTTTTTTTTT [-, T] GCTGTGCTTCTCTTTAGCGATTATGGCAAGTAAAGAGATTTGATTATCTTGTTC CTGTGAAAGGTTATTAGCCCTCAATCCCTTAAGTCACCTCTGCACTCCAGTGCAC GAGCCTCAGGTTATCAGCCAGGAAGAGTAATGGAGACACCAGGATCAGATTCTAAA GGAAGGAAAGTTAAAGCAAAGTTGAAAGGGGTGACAGCCAACAGCCATGAGCTTAGGAA CTCATTAGACTAAAAGACAACATCTCATTATCTGTTCCGAAATGATCTAAATACAT
84935	GAAGTTTATTTCCTGACTTTCAGATAAGCCCTGCAATGTCAACTTTGGAGGAAC TGGCTTGAGCTTGTAGTGTAGCAGCATTCAAGGAGTAGCAAGCACTAACAAACACAGGC ACTTGGAAAATGCGACTGCCAGTATTCTGAGCTAACCAAAACCTGATTGGACATCA AAGGTAGTATATATATTCAAAATAGTTCTCAATTGCAAAGTTGCAACCT AGAGTCTATATAATAGATTGCCAGCCAGGCCAGGCTCATGCCATGATCCAGCAC [C, T]

FIGURE 3FF

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

TTGGGAGGCTGAGGCAGGTGGATCACCTGAGGTAGGAGTTCAAGACCAGCCTGGCCAAC
GTGGTGAACCTTGTCCTCATTAAAATACAAAATTAGCCAGATGTGGTGTGCTTGC
TGTAGTCCCAGCTACTCGAGGCTGAGGAGAATCACTTGAACCCAGGAAGTGGAGG
CTGCAGTGAGCCGAGATCACCCACTGCACTCCAGCCTGGGCCACAGAGTGAAGACTCAGT
CTCAAAAAAAAGAAAAAAAAAAAGATTGCCTAATGTATCTAACAAAATTGGAAA

87476 AGATATCGGCTTCTGGCTCTTCTAACATCATTGTCTTGTCTCAAAGAGCAGGGAAAGTT
TAAAATTATAGCTGATCCTCAGAGCATTTATGAAATACCTAACGTTGTATTTGACAAT
ATACATTAGAATTACAATTGGTGATATAATATGGTATTTCCAAGCAAATATTCTCTA
GAGCAGAGCTTTACTGTATAATTATTAAACCTGCTAGTTATAAGGACAGAATGAACCT
TTAGCTGCATTCTGTGAAGTGGAGGGCCTTACCCCTCATAAAATTATCAAAGATACTAAT
[C, G]
GAAATGGGCTCAGATGGTGGTGTCCATTAACATTATTATTCTATTGTTTTATT
TATTTCTTAAGCAGCTGGAGGTAGGGAGATAACCTTGCTTCTGATCTACAGTGACC
TTCCACAAAAAATTGCTACCTGTAGACATAATTGGTCACAATAGAAAATCAATTAAATG
CAGCATGTCAAGCTTGTGGCTGCGCCAGCAATTGAAGAAGGGAGAAGGCAGATTTGCC
TCTGCTGGAGTAAGCTCATGATGTCCCTAGGCCTGGTACGAATGTAAGGAGATAAAACT

FIGURE 3GG